

GenCore version 5.1.1.6

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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:36:09 ; Search time 42 Seconds
(without alignments)

1184.383 Million cell updates/sec

Title: US-10-618-173-2

Perfect score: 2712

Sequence: 1 MMSRDTKTESQSQSGTSSSS.....ASTSSCSILPTSAEKRAKR 517

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	621	22.9	513	1 S43941	protein kinase DUN
2	593.5	21.9	374	1 S50193	Ca2+/calmodulin-de
3	591.5	21.8	370	1 S57347	Ca2+/calmodulin-de
4	575.5	21.2	821	1 A39616	protein kinase RAD
5	563.5	20.8	460	2 S58882	protein kinase Cds
6	560.5	20.7	301	1 A40811	myosin-light-chain
7	539.5	19.9	469	1 S17656	Ca2+/calmodulin-de
8	538	19.8	445	2 T43420	probable protein k
9	537	19.8	348	2 T37321	Ca2+/calmodulin-de
10	535	19.7	524	2 A45472	protein kinase (EC
11	534.5	19.7	474	1 TVRTCA	Ca2+/calmodulin-de
12	534.5	19.7	502	1 I52637	Ca2+/calmodulin-de
13	531	19.6	473	1 A53036	Ca2+/calmodulin-de
14	507.5	18.7	735	2 A53300	ribosomal protein
15	506	18.7	560	2 S51600	phosphorylase kina
16	503.5	18.6	735	2 I51901	ribosomal protein
17	501.5	18.5	414	2 JN0323	Ca2+/calmodulin-de
18	501.5	18.5	504	2 T10449	probable serine/th
19	501	18.5	512	1 JC1446	serine/threonine-s
20	498.5	18.4	724	1 B32571	ribosomal protein
21	498	18.4	608	2 T18445	hypothetical prote
22	494.5	18.2	516	1 JU0270	Ca2+/calmodulin-de
23	493.5	18.2	509	2 B44412	calmodulin-depende
24	493.5	18.2	530	2 D44412	Ca2+/calmodulin-de
25	492.5	18.2	473	1 S59941	serine/threonine-s
26	490	18.1	511	1 A56009	serine/threonine-s
27	488	18.0	512	2 T52633	serine/threonine-s
28	487	18.0	504	2 T38226	probable serine-th
29	484.5	17.9	542	2 T08777	probable protein k

30	484	17.8	918	1 I48719	protein kinase C (
31	480.5	17.7	310	2 B88640	protein K07A9.2 (i
32	479.5	17.7	518	1 B46619	Ca2+/calmodulin-de
33	479.5	17.7	518	1 S43845	Ca2+/calmodulin-de
34	479.5	17.7	527	1 A31908	Ca2+/calmodulin-de
35	479.5	17.7	556	2 JC5636	Ca2+/calmodulin-de
36	479	17.7	912	1 A53215	protein kinase C (
37	478.5	17.6	533	1 A34366	Ca2+/calmodulin-de
38	478.5	17.6	580	2 T40939	probable Ca-calmod
39	473.5	17.5	520	2 F85059	probable calcium d
40	471.5	17.4	512	2 T07788	probable serine/th
41	470.5	17.3	503	2 T51156	calcium dependent
42	470.5	17.3	752	1 A32571	ribosomal protein
43	469	17.3	472	2 B90100	SNF-related kinase
44	469	17.3	490	1 S71776	calcium-dependent
45	468	17.3	1142	2 S59359	GIN4 protein - ya

ALIGNMENTS

RESULT 1

S43941

protein kinase DUN1 (EC 2.7.1.1) - Yeast (Saccharomyces cerevisiae)

N:Alternate names: protein D2370; protein YDL101c

C:Species: Saccharomyces cerevisiae

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S43941; S67643; S67418; S72106

R:Zhou, Z.; Ellledge, S.J.

Cell 75, 1119-1127, 1993

A:Title: DUN1 encodes a protein kinase that controls the DNA damage response in yeast.

A:Reference number: S43941; MUID:94084787; PMID:8261511

A:Accession: S43941

A:Molecule type: DNA

A:Residues: 1-513 <ZHO>

A:Cross-references: UNIPROT:P39009; EMBL:L25548; NID:G435616; PIDN:AAA16324.1; PID:G43561

R:Ballesta, J.P.G.; Ramacha, M.; Soler-Mira, A.; Jimenez, A.; Garcia-Cantalejo, J.M.; Bo

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67629

A:Accession: S67643

A:Molecule type: DNA

A:Residues: 1-513 <BAL>

A:Cross-references: EMBL:274149; NID:G1431139; PIDN:CAA98668.1; PID:G1431140; GSPDB:GN00

A:Experimental source: Strain S288C

R:Bozkovic, J.; Saiz, J.E.; Soler-Mira, A.; Garcia-Cantalejo, J.; Revuelta, J.L.; Jimine

submitted to the EMBL Data Library, February 1996

A:Reference number: S67406

A:Accession: S67418

A:Molecule type: DNA

A:Residues: 1-513 <BOS>

A:Cross-references: EMBL:X95644; NID:G1199535; PIDN:CAA64912.1; PID:G1199548

R:Saiz, J.E.; Buitrago, M.J.; Garcia, R.; Revuelta, J.L.; del Rey, F.

Yeast 12, 1077-1084, 1996

A:Title: The sequence of a 20.3 kb DNA fragment from the left arm of Saccharomyces cerevi

A:Reference number: S72094; MUID:97051597; PMID:8896274

A:Accession: S72106

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-513 <SAI>

A:Cross-references: EMBL:X95644; NID:G1199535; PIDN:CAA64912.1; PID:G1199548

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996

C:Genetics:

A:Gene: SGD:DUN1; MIPS:YDL101c

A:Cross-references: MIPS:YDL101c; SGD:S0002259

A:Map position: 4L

C:Function:

A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine

C:Superfamily: protein kinase DUN1; kinase interaction domain homology; protein kinase h

C:Keywords: ATP; nucleus; phosphoprotein; phosphotransferase; serine/threonine-specific i

F:58-128/Domain: kinase interaction domain homology <KIH>

F:198-480/Domain: protein kinase homology <KIN>

F:206-214/Region: protein kinase ATP-binding motif

Query Match 22.9%; Score 621; DB 1; Length 513;
Best Local Similarity 32.1%; Pred.No.2.2e-21;
Matches 149; Conservative 73; Mismatches 152; Indels 90; Gaps 12;

QY 88 GRDKKCDYTDDIPVLTQTDRYKYTKSRKHFFRIQLFQELGHGHSRVANIEDLSNGCTFYVNKEII 147
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
59 GRGRSCDV-----ILSEPD-ISTFHAEFHLLQMDVDNFQRNLINVIDKS RNGTFINGNRL 112
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 148 GKGRTLPLTNABIALSLPTNKVFVF-----SDLSVDDQT----- 183
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
113 VK-KDYILKNGDRIVFGKSCSFLFKYASSSTDIENDDEKVSSESRSYKNDDVEFKKPOI 171
DB -----YPKDFIDKIYMSRPISGACGEVKLAPQKSVCKVAVKII 223
QY 172 SATSSQNATTSAAIRKLNTKTRPVSFDPKYLGLKELGAGHVALVKEAKNKKTQQQVAVKIF 231
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
224 SKRK---FKMNTSSNEHPISVDTEIELTKXLDHPCIK-----LENFFDESDFYIVLEL 275
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
232 HAQNDQKKNNKFRE-----ETNILMRVQHPIVNLNLDSPFEPSIQIKYILVLEK 284
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 276 MEGGELFDRVNVNSTRLRPEIAKLYFYOMLLAVOVLHENGVIHRDLKPENVLLSSTSEE-- 333
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
285 IDDGELFERIVKTCRLQRDSKALFKOLLTCLXYLHEQNIHREDIKPENILLNITRENTP 344
DB -----CCIKITDQGSKILTGETSLMRTLCGPPTYLABEVLTAGTTGYSSA 379
QY 334 -----SQVOLGPWDEIDEIOVKIADFGLAKFTGMQMFTNTLCGTPTSYVAPEVLT--KKGYTSK 401
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
380 VDCWSLGVLVFCVLCGVPPESQNSNIPLKNOAQEAGTYTIIAAARNVNSQAFLVKNLL 439
QY :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
402 VDWASAGVILVCLCGFPFSDQLGPPSLKEQILQAKYAFSPYPWDKIDDSVLHLISNLL 461
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 440 VVPDEORLRTTKQALEHPWLQD----DSMKHTVERLMYGVGDHTMP 479
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
462 VLNPDERYNIDEALNHPWFINDIQQSSVSLELQRLQI-TDNKIP 504
DB :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 2
S50193
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat
N;Alternate names: CAMKI
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S50193; A49682; A46038
R;Cho, F.S.; Phillips, K.S.; Bogucki, B.; Weaver, T.E.
Biochim. Biophys. Acta 1224, 156-160, 1994
A;Title: Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent protein kinase I.
A;Reference number: S50193; MUID:95035115; PMID:7948038
A;Accession: S50193
A>Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <CHO>
A;Cross-references: UNIPROT:Q63450; EMBL:L26288; NID:g439613; PIDN:AAA66944.1; PID:g439613
R;Picciotto, M.R.; Czernik, A.J.; Nairn, A.C.
J. Biol. Chem. 268, 26512-26521, 1993
A;Title: Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification
A;Reference number: A49682; MUID:94075341; PMID:8253780
A;Accession: A49682
A>Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-111,'G', 113-117,'R', 119-308,'R', 310-322,'HQPQ', 327,'T', 329,'TDS' <PIC>
R;Mochizuki, H.; Ito, T.; Hidaka, H.
J. Biol. Chem. 268, 9143-9147, 1993
A;Title: Purification and characterization of Ca2+/calmodulin-dependent protein kinase I.
A;Reference number: A46038; MUID:93232082; PMID:8386178
A;Accession: A46038
A>Status: preliminary
A;Molecule type: protein
A;Residues: 12-36,'T' <WOC>
A;Experimental source: cerebrium
C;Note: sequence extracted from NCBI backbone (NCBIP:129927)
C;Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology

C;Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransferase
F;18-276/Domain: protein kinase homology <KIN>
F;26-34/Region: protein kinase ATP-binding motif
F;293-299/Region: autoinhibitory
F;302-314/Region: calmodulin binding
F;177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

	Query Match	21.9%	Score 593.5;	DB 1;	Length 374;
	Best Local Similarity	39.9%;	Pred. No. 2.9e-20;	Mismatches 106;	Indels 19; Gaps 5;
	Matches 124;	Conservative 62;	Mismatches 106;	Indels 19;	Gaps 5;
Qy	186 KDFIDKYIMSPISGACGEVKLAFQSKVCKKVAVKIISKRFKMNTSSNEHPISVDTEI	245	:	:	:
Db	14 EDIRDIYDFRDVLGTGAFSEVILAEADKRTQKLVAIKIAKELEGEGSMEN-----EI	67	:	:	:
Qy	246 EILKKLDHPCIIKTENPFDSDFYYIVILELMGGELFDRVVNSTRLEPIAKLYFYQMLL	305	:	:	:
Db	68 AVLHKIKHPNVALDDIYESGGHLTYLMQLVSGGSLFDRIKVGFTTERDASRLIFQVLD	127	:	:	:
Qy	306 AVQYLHENGVIHRLDKPENLVLLSSTSECCIKITDFGOSKILGETSLMRTLCTPTFLAP	365	:	:	:
Db	128 AVKYLHDIGIVHRLDKPENLVLYSLDEDSKIMISDFGLSKMEDPGSVLTACGTPGVAP	187	:	:	:
Qy	366 EVLNTAGTGYSSA VDCWSLGVLFCVLCGYPFPFSEONSNIPLKNQIAEGKYTYIAAAWR	425	:	:	:
Db	188 EVL---AQPKYSKAVDCWSIGVIAYILLCGYPFPFDEN--DAKLFEQILKAIEYEFSDPYWD	243	:	:	:
Qy	426 NVSQAFPDLVGNLAVVDPEQRLLTTKQALEHPWLQDDSMKHVTVERLMYGVDHTMPPTKKN	485	:	:	:
Db	244 DISAKDPFIKHLMEKDFEKRFTCEALQHPWIAGDT-----ALDKNIHQSVSEQIKKN	297	:	:	:
Qy	486 IIRKRGHWDQ 496	:	:	:	:
Db	298 FAKSK---WKQ 305	:	:	:	:

RESULT 3
S57347
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human
N;Alternate names: CAMKI
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
R;Accession: S57347
R;Author: B.; Hook, S.S.; Selbert, M.A.; Goldstein, E.G.; Tonhave, E.D.; Edelman, A.M.; EMBO J. 14, 3679-3686, 1995
A;Title: Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain structure, expression, and functional characterization.
A;Reference number: S57347; MUID:95369239; PMID:7641687
A;Accession: S57347
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-370 <HAR>
A;Cross-references: UNIPROT:Q14012; EMBL:L41816; NID:g790789; PIDN:AAA99458.1; PID:g790789;
C;Genetics:
A;Gene: GDB:CAMKI
A;Cross-references: GDB:642249
C;Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
C;Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransferase
F;18-276/Domain: protein kinase homology <KIN>
F;26-34/Region: protein kinase ATP-binding motif
F;293-299/Region: autoinhibitory
F;302-314/Region: calmodulin binding
F;177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

	Query Match	21.8%	Score 591.5;	DB 1;	Length 370;
	Best Local Similarity	39.9%;	Pred. No. 3.5e-20;	Mismatches 107;	Indels 19; Gaps 5;
	Matches 124;	Conservative 61;	Mismatches 107;	Indels 19;	Gaps 5;
Qy	186 KDFIDKYIMSPISGACGEVKLAFQSKVCKKVAVKIISKRFKMNTSSNEHPISVDTEI	245	:	:	:
Db	14 EDIRDIYDFRDVLGTGAFSEVILAEADKRTQKLVAIKIAKELEGEGSMEN-----EI	67	:	:	:
Qy	246 EILKKLDHPCIIKTENPFDSDFYYIVILELMGGELFDRVVNSTRLEPIAKLYFYQMLL	305	:	:	:

A;Title: S-phase specific activation of Cds1 kinase defines a subpathway of the checkpoint
A;Reference number: Z26084; MUID:98119835; PMID:9450932
A;Accession: T52473
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-202, 'I', 204-237, 'F', 239-460 <LIN>
A;Cross-references: EMBL:A0222869; NID:g2689196; PIDN:CAAL1019.1; PID:g2689197
C;Genetics:
A;Gene: SPBC18B5.11C; cds1
A;Map position: 3
A;Introns: 86/3; 103/1; 113/3; 142/1; 228/3; 298/3; 368/2
C;Function:
A;Description: EC 2.7.1.-; protein kinase Cds1 [validated, MUID:98119835]; is required for S-phase arrest and activated by S-phase arrest and activated by DNA damage
A;Note: Cds1 is phosphorylated and activated by S-phase arrest and activated by DNA damage
C;Superfamily: protein kinase Cds1; kinase interaction domain homology; protein kinase H
C;Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;62-133/Domain: kinase interaction domain homology <KIN>
F;165-433/Domain: protein kinase homology <KIN>
F;173-181/Region: protein kinase ATP-binding motif
Query Match 20.8%; Score 563.5; DB 2; Length 460;
Best Local Similarity 33.3%; Pred. No. 7.8e-19;
Matches 144; Conservative 75; Mismatches 163; Indels 51; Gaps 13;
QY 87 FGRDKKCDYTFDIPVLNQTDRYKTYSKRHRIFQELGHG-----SRVANIEDLSNGTFF 141
DB 62 FGRHKSCEVLNCP-----RVSNPFHFYIQ--GHRNDSDESENVVFLHDHSSNGTFF 110
QY 142 VNKEILIGKRTPLTNAAE--TALSPTNKFVFDLSV-----DDQTYPKDFIDKYIMS 195
DB 111 LNFERLAKNSRTLNSGDBIRIGLGVPKDEISFLCQVPVHKSRDSQKNMKSNSHYEII 170
QY 196 RPIGSGACGEVKLAFQSKVCKVAVKIISKRFKMTSSNEHPISVDTEIETILKLDHPC 255
DB 171 RILSGSTFAVKLAVENVSKVYAKIINKRKLITSEKRATEMFORDEIDILKSLHHPG 230
QY 256 IIKIENFFDSDFYIVLELMGEGELFDRVNVSTRLEPIAKLYFYQMLLAVQYLHENG 315
DB 231 VVQCHEICENDELFIWMEYVEGDLDFLIANGSIDEQCKPLKQLLETLLHLKQGV 290
QY 316 IHRDLKPNVLSSSECCIKITDFGQSKIL-GETSLMRTLCTGPTTYLAEVLTAGTT 374
DB 291 THRDLKPNILTN--DFHLKISDFGLAKVTHGTFTLETFCGTMGLAPEVLKSKNVN 347
QY 375 ---GYSSAVDCWSLGVILFVCLCGVPPF--SQNSNIPLNKQIARGKTYTIAAAWNVSE 429
DB 348 LDGGYDDKVDIWSLGCVLVYMLTASIPFASSQAKCIEL---ISGAYPIEPLENEISE 404
QY 430 QAFDLVKNLLVVDPEQRLLTKQALEHPMLQDDSMKHTVERLMYGVDMTPPPPIKKNIRK 489
DB 405 EGIDLINRMLEINPEKRISSEALQHPWF-----YTVST---HEHRTPPSSSE----- 449
QY 490 RGHWDQDASTSS 502
DB 450 --HEATEQLNSSS 460
RESULT 6
A40811
N;Title: myosin-light-chain kinase (EC 2.7.1.117) A - slime mold (Dictyostelium discoideum)
N;Alternate names: MLCK-A
C;Species: Dictyostelium discoideum
C;Date: 10-Apr-1992 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C;Accession: A40811; A37125
R;Tan, J.L.; Spudich, J.A.
J. Biol. Chem. 266, 16044-16049, 1991
A;Title: Characterization and bacterial expression of the Dictyostelium myosin light chain
A;Reference number: A40811; MUID:91340753; PMID:1651931
A;Accession: A40811
A;Molecule type: mRNA
A;Residues: 1-301 <TAN>
A;Cross-references: UNIPROT:P25323; GB:M64176; NID:gl490249; PIDN:AAB06337.1; PID:gl4982
R;Tan, J.L.; Spudich, J.A.

J. Biol. Chem. 265, 13818-13824, 1990
A;Title: Dictyostelium myosin light chain kinase. Purification and characterization.
A;Reference number: A37125; MUID:90337997; PMID:2380188
A;Accession: A37125
A;Molecule type: protein
A;Residues: 9-12, 'I', 14-19; 163-167, 'S', 169-179; 192-198 <TA2>
C;Genetics:
A;Gene: mlka
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine in itself
A;Pathway: cytokinesis; fruiting body formation
A;Note: not activated by Ca2+/calmodulin in contrast with MLCK from higher eukaryotes
C;Superfamily: kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; autophosphorylation; cell division; phosphoprotein; phosphotransferase;
F;6-265/Domain: protein kinase homology <KIN>
F;14-22/Region: protein kinase ATP-binding motif
F;1267-295/Domain: inhibitory #status predicted <INH>
F;37/Active site: Lys #status predicted
F;296/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted
Query Match 20.7%; Score 560.5; DB 1; Length 301;
Best Local Similarity 38.7%; Pred. No. 7.1e-19;
Matches 116; Conservative 58; Mismatches 105; Indels 21; Gaps 5;
QY 192 YIMSRPIGSGACGEVKLAFQSKVCKVAVKIISKRFKMTSSNEHPISVDTEIETILK 251
DB 8 YEFKEELGRGAFSVYIYLGKNTQKQRYAKVINKSELGKDYEK-----LKNVEDILKKV 62
QY 252 DHPCHIKIENFFDSDFYIVLELMGEGELFDRVNVSTRLEPIAKLYFYQMLLAVQYLH 311
DB 63 NHPNIIALKELFDTPKLYLVMLVETGGLFDPKIVKGVSEADAANLVKKIVSAVGYLH 122
QY 312 ENGVIHRDLKPNVLSSSECCIKITDFGQSKILGETSLMRTLCTGPTTYLAEVLTNTA 371
DB 123 GLNIVHRDLKPNVLSSSECCIKITDFGQSKILGETSLMRTLCTGPTTYLAEVLTNTA 371
QY 372 GTTGYSSAVDCWSLGVILFVCLCGVPPFSEQNSNIP-LKNQIARGKTYTIAAAWNVSEQ 430
DB 181 -ATGYDEKVDWMSIGVITYILLCCGFPF--YGDVTFEIPFQIMVNVFEPPEYWGGSKE 237
QY 431 AFDLVKNLLVVDPEQRLLTKQALEHPMLQDDSMKHTVERLMYGVDMTPPPPIKKNIRK 490
DB 238 AKDFIGKLLVVDVSKRLNATNALNHPMLKSNNSNTIDTV-----KMKYEVIVERR 287
RESULT 7
S17656
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S17656; A29878; I49571
R;Jones, D.A.; Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikela, J.M.
FEBS Lett. 289, 105-109, 1991
A;Title: cDNA sequence and differential expression of the mouse Ca(2+)/calmodulin-depende
A;Reference number: S17656; MUID:91372388; PMID:1893997
A;Accession: S17656
A;Molecule type: mRNA
A;Residues: 1-469 <JON>
A;Cross-references: UNIPROT:P08414; EMBL:X58995; NID:g50366; PIDN:CAA41741.1; PID:g50367
R;Sikela, J.M.; Hahn, W.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 3038-3042, 1987
A;Title: Screening an expression library with a ligand probe: isolation and sequence of
A;Reference number: A29878; MUID:87204263; PMID:3033675
A;Accession: A29878
A;Molecule type: mRNA
A;Residues: 315-469 <SIK>
A;Cross-references: GB:M16206; NID:g200360; PIDN:AAA39933.1; PID:g387512
R;Sikela, J.M.; Law, M.L.; Kao, F.
Genomics 4, 21-27, 1989
A;Title: Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent I
A;Reference number: I49571; MUID:09122027; PMID:2536634
A;Accession: I49571

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 250-277; 'CRGI', 281-301, 'T', 303-338, 'X', 340-469 <RES>
A:Cross-references: GB:J030057; NID:g192366; PIDN:AAA37366.1; PID:g192367
A:Experimental source: brain
C:Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology
C:Keywords: ATP; calmodulin binding; phosphotransferase; serine/th
F:40-296/Domain: protein kinase homology <KIN>
F:48-56/Region: protein kinase ATP-binding motif
F:306-469/Product: calpermin #status predicted <GSP>
F:318-337/Region: calmodulin binding #status predicted
F:71/Active site: Lys #status predicted

Query Match 19.9%; Score 539.5; DB 1; Length 469;
Best Local Similarity 39.8%; Pred. No. 9.6e-18;
Matches 117; Conservative 53; Mismatches 103; Indels 21; Gaps 3;

QY 174 SLSVDDQTIYKDFDK-----YIMSRPIGSGACGEVKLAFQKSVCKKAVKIIS 224
DB 15 SSVTASTENLVDYWDGNSRDLGDFVESELGRGATSIYVRCKQKGTQKPYALKVLK 74

QY 225 KRKFKMNTSSNEHPIVDTEIEILKKLDHPCIIKIENPFDSDFYIVILELMEGGELFDR 284
DB 75 KTVDKK-----IVRTEIGVLLRSLSHPNIIKLEIFETPTSEISLVLELVTGGELFDR 125

QY 285 VVNSTRLEPIAKLYQMLLAVOYLHENGVIHRLDKPENVLSSSTSECCIKITDFGQS 344
DB 126 IVEKGYISERDARDVAKQLLEAVAYLHENGVIHRLDKPENLILYATPAPAPLKIADFGLS 185

QY 345 KILGETSLMRTLCGTYLAPELVNTAGTYGSSAVDCWSLGVILFVLCGYPFPSEQNS 404
DB 186 KIVEHQVLMTKVTGTPGYCAPELTRGC---AYGPEVDMWSVGLIITVILCGPEPFYDERG 242

QY 405 NIPLKNQIAEGKYTYIAAARNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWL 458
DB 243 DQFMFPRILNCEYFISPWDESLNAKDLVKLIVLDPKKRLTTFQALQHPWV 296

RESULT 8
T3420
Probable protein kinase (EC 2.7.1.-) mek1 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 16-Aug-2004
C:Accession: T43420; T37688
R:lyne, M.H.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z22503
A:Accession: T43420
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-445 <LYN>
A:Cross-references: UNIPROT:Q10292; EMBL:Z71478; PIDN:CAA96101.1
A:Experimental source: strain 972h(-)
R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21737
A:Accession: T37688
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-445 <DEV>
A:Cross-references: EMBL:Z98596; PIDN:CA11196.1; GSPDB:GN00066; SPDB:SPAC14C4.03
A:Experimental source: strain 972h-; cosmid c14C4
C:Genetics:
A:Gene: mek1; SPAC14C4.03
A:Map position: 1
A:Introns: 53/1; 231/2
C:Superfamily: protein kinase homology
C:Keywords: phosphotransferase

Query Match 19.8%; Score 538; DB 2; Length 445;
Best Local Similarity 31.9%; Pred. No. 1.1e-17;
Matches 146; Conservative 72; Mismatches 182; Indels 58; Gaps 15;

QY 29 SQSSSGTSLSSLDITVPVQDLASIPRDEIDIPQWGRLWALGKG-----FLNHDCLHEE 84
DB 10 SRSESTQILCELSQIDESTM-----DPQYTED--DVLARLFVSSSSPQTVLNVK- KYBD 61

QY 85 YVFGDKKCDYTFDIPVLNQDTRYKYSKRHFRIQEL-GHGHSRVANETDLSGNGTFVN 143
DB 62 VSVGRSNTCY-----QLQFTASYK-----HPRVSVLIDDDMDPLVYCEDOSSNGTFLN 112

QY 144 KEIIIGKRTPLPTNNAEIALSLPTNKVVFSDLSVDDQTIYKDFIDKY-----IMSRP 197
DB 113 HRLICKGNV-LLSDGDI-LDVRHCASFLOQKYTTD-----NDFHHEYAGERFNITQRL 165

QY 198 TSGACGEVKLAFQKSVCKKAVKIIISRKFKMNTSSNEHPIVDTEIEILKKLDHPCII 257
DB 166 LGIGGFSRIYAMDNMTGGYACKIIDKKISTKRFEDH-----EMTILKLDHPNII 219

QY 258 KIENFDSDFYIVILELMEGGELFDRVNVNSTRLEPIAKLYQMLLAVOYLHENGVIH 317
DB 220 KVMYENSETOFFIEEMVTGDLFSYLTGKLTGVPVTVTLFIMFQLQGLKYLHQNIH 279

QY 318 RDLKPEVLLSSTSECC- IKITDFGQS KILGETSLMRTLCGTYLAPELVNTAG- --- 372
DB 280 RDLKLENILIASSTDITFRILITDFGVARCQKQKRLSTFVGTPEYTAPEIQRLKGRSQV 339

QY 373 ---TTGYSADVCSLGVILFVLCGYPFPSEQNSNPLKNQIAEGKYTYIAAARNVVS 428
DB 340 EKENSNGYKGVLDLSLGVIMFLLLSGNSP-----SFADGVKEKQVDFRDPVWKSVS 391

QY 429 EQADPLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHT 466
DB 392 RQAKDLISNLLNTPDRPTVKQCLSHPFARHSSRLT 429

RESULT 9
T37321
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T37321
R:Eto, K.; Takahashi, N.; Kimura, Y.; Masuho, Y.; Arai, K.; Muramatsu, M.; Tokumitsu, H.
J. Biol. Chem. 274, 22556-22562, 1999
A>Title: Ca2+/calmodulin-dependent protein kinase cascade in Caenorhabditis elegans. Imp
A:Reference number: Z21686; MUID:99357789; PMID:10428833
A:Accession: T37321
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-348 <ETO>
A:Cross-references: UNIPROT:Q9UAH6; EMBL:AB021864; NID:g5672677; PIDN:BAA82674.1; PID:g56
A:Experimental source: strain Bristol N2; embryonic stage
C:Genetics:
A:Note: cmk-1
C:Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology
C:Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransfer

Query Match 19.8%; Score 537; DB 2; Length 348;
Best Local Similarity 39.2%; Pred. No. 9.4e-18;
Matches 118; Conservative 60; Mismatches 105; Indels 18; Gaps 6;

QY 190 DKYIMSRPIGSGACGEVKLAFQKSVCKKV-AVKIISKRFKMNNTSSNEHPIVDTEIEIL 248
DB 20 EKYDFRDLVLTGTFGAFSKVLAESKSDAGQYAVKIDKKALGKKE-----SLENEIKVL 73

QY 249 KKLDHPCIIKIENPFDSDFYIVILELMEGGELFDRVNVNSTRLEPIAKLYQVQMLLAVQ 308
DB 74 RKLHNNIVQLFDYDEKQFVYLVMELVTGGELFDRIVAKGSYTTQDASNLIRQVLEAVG 133

QY 309 YLHENGVIHRLDKPENVLSSSTSECCIKITDFGQS KILGETSLMRTLCGTYLAPEVL 368
DB 134 FMHNGVVRDLKPENLILYQDDESKIMISDFGLSK-TEDSGVWATACGTPGYVAPEVL 192

QY 369 NTAGTGTGYSADVCSLGVILFVLCGYPFPSEQNSNPLKNQIAEGKYTYIAAARNVVS 428
DB 193 Q---QKPYGKAVDWSIGVIAYIILCGYPPFYDE-SDANLFAQITIKGSEYFADPYWDQIS 248

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:34:23 ; Search time 178 Seconds
(without alignments)
1487.331 Million cell updates/sec

Title: US-10-618-173-2

Perfect score: 2712

Sequence: 1 MMSRDTKTESQSQGTSSSS.....ASTSSCEILPTSAEKRAKR 517

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_03.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2712	100.0	517	Q918V3	Q918V3 xenopus lae
2	2704	99.7	517	Q98TW0	Q98TW0 xenopus lae
3	1655.5	61.0	543	1 CHK2_HUMAN	Q96017 homo sapien
4	1644.5	60.6	545	2 Q9R019	Q9R019 rattus norv
5	1637	60.4	546	1 CHK2_MOUSE	Q92265 mus musculu
6	1624	59.9	586	2 Q6QA11	Q6QA11 homo sapien
7	1499	55.3	514	2 Q9HCQ8	Q9HCQ8 homo sapien
8	1317.5	48.6	503	2 Q90Z15	Q90Z15 brachydanio
9	1311.5	48.4	503	2 Q803E2	Q803E2 brachydanio
10	1287	47.5	452	2 Q6QA05	Q6QA05 homo sapien
11	1066	39.3	322	2 Q9HBS5	Q9HBS5 homo sapien
12	1012.5	37.3	339	2 Q6QA08	Q6QA08 homo sapien
13	828	30.5	476	1 LOK_DROME	O61267 drosophila
14	791	29.2	289	2 Q6QA10	Q6QA10 homo sapien
15	727.5	26.8	712	2 Q7SEK0	Q7SEK0 neurospora
16	644.5	23.8	443	2 Q6BH59	Q6BH59 debaryomyce
17	621.5	22.9	476	1 CHK2_CAEEL	Q9ULY5 caenorhabdi
18	621	22.9	513	1 DUNI_YEAST	P39009 sacharomyc
19	619.5	22.8	506	2 Q6FKZ8	Q6FKZ8 candida gla
20	610.5	22.5	378	2 Q8AVN4	Q8AVN4 xenopus lae
21	605	22.3	472	2 Q9XTX3	Q9XTX3 caenorhabdi
22	603	22.2	469	2 Q9HBS5	Q9HBS5 ashbya goss
23	602.5	22.2	388	2 Q64HW3	Q64HW3 oncorhynch
24	600.5	22.1	357	2 Q9HD31	Q9HD31 homo sapien
25	600.5	22.1	367	2 Q8BW17	Q8BW17 mus musculu
26	600.5	22.1	385	2 Q8IU85	Q8IU85 homo sapien
27	600.5	22.1	385	2 Q8BW96	Q8BW96 mus musculu
28	599.5	22.1	382	2 Q8AYR2	Q8AYR2 xenopus lae
29	595.5	22.0	377	2 Q8OW64	Q8OW64 mus musculu
30	595.5	22.0	415	2 Q6CPX0	Q6CPX0 kluyveromyc
31	593.5	21.9	374	1 KCCL_MOUSE	Q91Y88 mus musculu

ALIGNMENTS

RESULT 1

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Q918V3
ID Q918V3 PRELIMINARY; PRT; 517 AA.
AC Q918V3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Protein kinase Cdelta.
GN Name=Cdelta;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP MEDLINE=20255216; PubMed=10793133;
RA Guo Z., Dunphy W.G.;
RT "Response of Xenopus Cdelta in cell-free extracts to DNA templates with
double-stranded ends."
RL Mol. Biol. Cell 11:1535-1546(2000).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF174295; AAF75829.1; -.
DR HSSP; O96017; IGXC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR008984; SMAD_FHA.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00669; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50006; FHA_DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 517 AA; 58261 MW; 39DC05689090DB19 CRC64;
```

Query Match 100.0%; Score 2712; DB 2; Length 517;

Best Local Similarity 100.0%; Pred. No. 1.4e-164; Indels 0; Gaps 0;

Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSRDTKTESQSQGTSSSSSSAPQSYSSSSSGTSLSLDTPVPQDLASIFDEPDED 60

DB 1 MMSRDTKTESQSQGTSSSSSSAPQSYSSSSSGTSLSLDTPVPQDLASIFDEPDED 60

QY 61 IPQPWGRWLWLGKGFNLHNDLHEEYVFGDKCDYTFDIPVLNQTDTRYKTSKRHFRIQ 120

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Db 61 IPQWGRWALWKGFLNHDCLHEEVFGDRDKKCDYTFDIPVLNQTDRTYKTSKRHFRIQ 120
Qy 121 ELGHGHSRVANIEDLSNGTGFVNKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
Db 121 ELGHGHSRVANIEDLSNGTGFVNKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
Qy 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKVAVKIIISKRKFQMTSSNEHPIS 240
Db 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKVAVKIIISKRKFQMTSSNEHPIS 240
Qy 241 VDTTEILKLDHPICIIKIENPFDSDFYIIVLELMEGELFDRVNVNSTRLEPIAKLYF 300
Db 241 VDTTEILKLDHPICIIKIENPFDSDFYIIVLELMEGELFDRVNVNSTRLEPIAKLYF 300
Qy 301 YQMLLAQVYLHENGVIHRDLKPNVLLSTSECCIKITDFQSKILGETSLMRTLCTGP 360
Db 301 YQMLLAQVYLHENGVIHRDLKPNVLLSTSECCIKITDFQSKILGETSLMRTLCTGP 360
Qy 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSIPLKNQIAEGKYTYI 420
Db 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSIPLKNQIAEGKYTYI 420
Qy 421 AAARNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVVHTWPP 480
Db 421 AAARNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVVHTWPP 480
Qy 481 PIKKNIIIRKRGHEWDQDASTSSCSSEILPTSAEKRKR 517
Db 481 PIKKNIIIRKRGHEWDQDASTSSCSSEILPTSAEKRKR 517
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RESULT 2

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Q98TW0 PRELIMINARY; PRT; 517 AA.
AC Q98TW0;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Protein kinase Cdel.
GN Name=Cdel;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]_TaxID=8355;
RP SEQUENCE FROM N.A.
RA Matsui T., Nakanishi M., Takisawa H.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF326574; RAG59884.1; -.
DR HSSP; O96017; IGXC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR008984; SMAD_FHA.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00699; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50006; FHA_DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 517 AA; 59310 MW; 401A3235AA0BDCBE CRC64;
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Query Match 99.7%; Score 2704; DB 2; Length 517;
Best Local Similarity 99.8%; Pred. No. 4.5e-164;
Matches 516; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MMSRDTKTESQOQSGTSSSSSSAPQSYSSQSSSGTSSSLDTPVQDLASIPEDPEIDED 60
Db 1 MMSRDTKTESQOQSGTSSSSSSAPQSYSSQSSSGTSSSLDTPVQDLASIPEDPEIDED 60
Qy 61 IPQWGRWALWKGFLNHDCLHEEVFGDRDKKCDYTFDIPVLNQTDRTYKTSKRHFRIQ 120
Db 61 IPQWGRWALWKGFLNHDCLHEEVFGDRDKKCDYTFDIPVLNQTDRTYKTSKRHFRIQ 120
Qy 121 ELGHGHSRVANIEDLSNGTGFVNKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
Db 121 ELGHGHSRVANIEDLSNGTGFVNKEIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
Qy 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKVAVKIIISKRKFQMTSSNEHPIS 240
Db 181 QTIYPKDFIDKYIMSRPIGSGACGEVKLAFQSVCKVAVKIIISKRKFQMTSSNEHPIS 240
Qy 241 VDTTEILKLDHPICIIKIENPFDSDFYIIVLELMEGELFDRVNVNSTRLEPIAKLYF 300
Db 241 VDTTEILKLDHPICIIKIENPFDSDFYIIVLELMEGELFDRVNVNSTRLEPIAKLYF 300
Qy 301 YQMLLAQVYLHENGVIHRDLKPNVLLSTSECCIKITDFQSKILGETSLMRTLCTGP 360
Db 301 YQMLLAQVYLHENGVIHRDLKPNVLLSTSECCIKITDFQSKILGETSLMRTLCTGP 360
Qy 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSIPLKNQIAEGKYTYI 420
Db 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSIPLKNQIAEGKYTYI 420
Qy 421 AAARNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVVHTWPP 480
Db 421 AAARNVSEQAFDLVKNLLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVVHTWPP 480
Qy 481 PIKKNIIIRKRGHEWDQDASTSSCSSEILPTSAEKRKR 517
Db 481 PIKKNIIIRKRGHEWDQDASTSSCSSEILPTSAEKRKR 517
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RESULT 3

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CHK2 HUMAN
ID CHK2 HUMAN STANDARD; PRT; 543 AA.
AC O96017; Q9UGF0; Q9UGF1;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serine/threonine-protein kinase Chk2 (EC 2.7.1.37) (Cdel).
GN Name=CHK2; Synonyms=CHK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99108191; PubMed=9889122; DOI=10.1016/S0960-9822(99)80041-4;
RA Blasina A., van de Weyer I., Laus M.C., Luyten W.H.M.L., Parker A.E.,
RA McGowan C.H.;
RT "A human homologue of the checkpoint kinase Cdel directly inhibits
RT Cdc25 phosphatase.";
RL Curr. Biol. 9:1-10(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99055399; PubMed=9836640; DOI=10.1126/science.282.5395.1893;
RA Matsuo S., Huang M., Elledge S.O.;
RT "Linkage of ATM to cell cycle regulation by the Chk2 protein kinase.";
RL Science 282:1893-1897(1998).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=99199255; PubMed=10097108; DOI=10.1073/pnas.96.7.3745;
RA Brown A.L., Lee C.-H., Schwarz J.K., Mitiku N., Plwnica-Worms H.,
```

RA Chung J.H.;
RT "A human Cdc1-related kinase that functions downstream of ATM protein
in the cellular response to DNA damage.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:3745-3750(1999).
RN [4c]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon carcinoma;
RA Shao R.-G., Zhang H., Yu Q., Pommier Y.;
RT "Chk2/Rad51 cell cycle checkpoint protein kinase from human colon
carcinoma HT29 cells: regulation by autophosphorylation and DNA-
dependent protein kinase and inhibition by cell cycle regulatory
drugs.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=20057165; PubMed=10591208; DOI=10.1038/990031;
RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M.,
RA Clump M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K.,
RA Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,
RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J.,
RA Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G.,
RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,
RA Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Karshaw J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leversha M.A., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mccann O.T.,
RA Mcclay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsay H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M.,
RA Vaudin M., Walli M., Wallis J.M., Whiteley M.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard R., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Minoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T.,
RA Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L.W., Mardis E., Waterston R.,
RA Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S.,
RA Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E.,
RA Edelmann L., Kim U.J., Shizuya H., Simon M.I., Dumanski J.P.,
RA Peyrard M., Kedra D., Seroussi E., Fransson I., Tapia I., Bruder C.E.,
RA O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X.,
RA Khan A.S., Lane L., Tilahun Y., Wright H.;
RT "The DNA sequence of human chromosome 22.";
RL Nature 402:489-495(1999).
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP VARIANT THR-157, AND VARIANT COLON CANCER TRP-145.
RX MEDLINE=20085462; PubMed=10617473; DOI=10.1126/science.286.5449.2528;
RA Bell D.W., Varley J.M., Szydlo T.E., Kang D.H., Wahrer D.C.R.,
RA Shannon K.E., Lubratovich M., Versalis S.J., Iselbacher K.J.,
RA Fraumeni J.F., Birch J.M., Li F.P., Garber J.E., Haber D.A.;
RT "Heterozygous germ line hCHK2 mutations in Li-Fraumeni syndrome.";
RL Science 286:2528-2531(1999).
RN [8]
RP VARIANT THR-157.
RX PubMed=11461078; DOI=10.1054/bjoc.2001.1858;
RA Allinen M., Huusko P., Mantyniemi S., Launonen V., Winqvist R.;
RT "Mutation analysis of the CHK2 gene in families with hereditary breast
cancer.";
RL Br. J. Cancer 85:209-212(2001).
RN [9]
RP VARIANTS OSTEOSARCOMA SER-17 AND LEU-85.
RX PubMed=11746983; DOI=10.1002/gcc.1207;
RA Miller C.W., Ikezoe T., Krug U., Hofmann W.K., Tavor S., Vegesna V.,
RA Tsukasaki K., Takeuchi S., Koefler H.P.;
RT "Mutations of the CHK2 gene are found in some osteosarcomas, but are
rare in breast, lung, and ovarian tumors.";
RL Genes Chromosomes Cancer 33:17-21(2002).
RN [10]
RP VARIANTS PROSTATE CANCER LYS-64; PRO-145; ARG-167; CYS-180; HIS-180;
CYS-181; HIS-181; LYS-239; PHE-251; HIS-318; PRO-323; CYS-327 AND
LYS-476, AND VARIANT THR-157.
RX PubMed=12533788;
RA Dong X., Wang L., Taniguchi K., Wang X., Cunningham J.M.,
RA McDonnell S.K., Qian C., Marks A.F., Slager S.L., Peterson B.J.,
RA Smith D.I., Chevillier J.C., Blute M.L., Jacobsen S.J., Schaid D.J.,
RA Tindall D.J., Thibodeau S.N., Liu W.;
RT "Mutations in CHK2 associated with prostate cancer risk.";
RL Am. J. Hum. Genet. 72:270-280(2003).
CC -!- FUNCTION: Controls cell cycle checkpoint. May participate in
transduction of the DNA damage and replicational stress signals.
CC -!- Inhibits CDC25C phosphatase by phosphorylating it on Ser-216,
preventing the entry into mitosis. May have a role in meiosis as
well.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ENZYME REGULATION: Kinase activity is up-regulated by
autophosphorylation. Rapidly phosphorylated in response to DNA
damage and to replication block.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: High expression is found in testis, spleen,
colon and peripheral blood leukocytes. Low expression is found in
other tissues.
CC -!- DISEASE: Defects in CHK2 are associated with Li-Fraumeni syndrome
(LFS) [MIM:151623]; a highly penetrant familial cancer phenotype
usually associated with inherited mutations in p53/TP53.
CC -!- DISEASE: Defects in CHK2 are found in some patients with prostate
cancer (Cap) [MIM:176807].
CC -!- DISEASE: Defects in CHK2 are found in some patients with
osteosarcoma (OSR) [MIM:259500].
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1
subfamily.
CC -!- SIMILARITY: Contains 1 FHA domain.
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the European Bioinformatics Institute. There are no restrictions on its
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CC -----
DR EMBL; AF131197; CAAL0319.1; -
DR EMBL; AF086904; AAC83693.1; -
DR EMBL; AF096279; AAD11784.1; -
DR EMBL; AF174135; AAD48504.1; -
DR EMBL; AL117330; CAB62923.1; -
DR EMBL; AL121825; CAB62922.1; -
DR EMBL; BC004207; AAO4207.1; -
DR PDB; 1GXC; X-ray; A/D/G/J=64-212.
DR Genew; HGNC:16627; CHEK2.
DR H-InVDB; HIX0016341; -
DR Reactome; O96017; -
DR MIM; 604373; -
DR MIM; 151623; -
DR MIM; 176807; -
DR MIM; 259500; -
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; TAS.
DR GO; GO:0000077; P:DNA damage response, signal transduction re. .; TAS.
DR GO; GO:0006974; P:response to DNA damage stimulus; TAS.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.

Query Match 61.0%; Score 1655.5; DB 1; Length 543;
Best Local Similarity 59.9%; Pred. No. 2.9e-97;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;

QY 2 MSRDTKTESQ-----QSQTSSSSSSSAP-QSYSSSSSSSGLT 37
DB 1 MSRESDEAQQHGSSACQPHGVTQSQSSSQSGTSSSTSTWPNSSQSSSSSGLT 60
QY 38 SSLDTPVQDLASI-----PEDEDEDIPQWGLWALGKGFNLHDCHEEYVGRKK 92
DB 61 SSLETSTQELYSIPEDQBPQEPPEPTAPWALWALQDGFANLECVNDNYWGRDKS 120
QY 93 CDYTDIPVNLQDRTYKTSKHFRIQBELGHGSRVANIENLNGTFFVKEIIGKRT 152
DB 121 CHYCFDEPLKKTDKYRTYSKHFRIQBELGHGSRVANIENLNGTFFVKEIIGKRT 180
QY 153 LPLTNNAEIALSLPTNKVFVSDLSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
DB 181 RPLNNSEIALSLRNKVFVFDLTVDQSVYFKALRDEYIMSKTGLSGACGEVKLAFER 240
QY 213 SVCKVAVKIIISKRKFKNMSSNEHP-ISVDTEIELKLHPCIIKIENFPDSEDFYI 271
DB 241 KTCKKVAIKIIISKRKFKNMSSNEHP-ISVDTEIELKLHPCIIKIENFPDSEDFYI 299
QY 272 VLELMEGGELFDRVNVNSTRLREPIAKLYQYQMLLAVQYLHENGVIHRDLKPNVLLSSTS 331
DB 300 VLELMEGGELFDRVNVNKKELKATCKLYQYQMLLAVQYLHENGVIHRDLKPNVLLSQE 359
QY 332 BECCIKITDFGQSKILGETSLMRTLCGPTLYLAPEVLNTAGTGYSSAVDCWMSLVILFV 391
DB 360 EDCLIKITDFGSKILGETSLMRTLCGPTLYLAPEVLNSVGTAGYNAVDCWMSLVILFI 419
QY 392 CLCGYPPPPSEQNSNPLKKNQIAEGKYTYIAAARNVSEQAFLVKNLLVDPQRLTTQK 451
DB 420 CLSGYPPPPSEHRTQVSLKDQITSGKNYFIPVMAEVSEKALDLVKKLAVDPKARFTTEE 479
QY 452 ALEHPLWQDMSKHTVERLMYGVDMTPPP-----IKNNIRKRGHEWDDQDASTSS-----C 503
DB 480 ALRHPWLQEDMKRFQDLSEENESTALPQVLAQPSRKRKRPRGEAEGAEITTKRPVAC 539
QY 504 SEIL 507
DB 540 AAVL 543

RESULT 4
Q9R019

ID Q9R019 PRELIMINARY; PRT; 545 AA.
AC Q9R019;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Checkpoint kinase CHK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RX MEDLINE=99361938; PubMed=10435585; DOI=10.1038/sj.onc.1202925;
RA Chaturvedi P., Eng W.K., Zhu Y., Mattern M.R., Mishra R., Hurler M.R.,
RA Zhang X., Annan R.S., Lu Q., Faucette L.P., Scott G.F., Li X.,
RA Carr S.A., Johnson R.K., Winkler J.D., Zhou B.B.;
RT "Mammalian CHK2 is a downstream effector of the ATM-dependent DNA
RT damage checkpoint pathway."
RL Oncogene 18:4047-4054(1999).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF134054; AAD55890.1; -
DR HSP; O96017; 1GXC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR008984; SMAD_FHA.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00069; Kinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SMO0240; FHA; 1.
DR SMART; SMO0220; S_TKc; 1.
DR PROSITE; PS00006; FHA DOMAIN; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 545 AA; 60930 MW; CE532BAD08608873 CRC64;
Query Match 60.6%; Score 1644.5; DB 2; Length 545;
Best Local Similarity 63.0%; Pred. No. 1.5e-96;
Matches 327; Conservative 69; Mismatches 108; Indels 15; Gaps 7;
QY 3 SRDTKTESQ-----QSQTSSSSSSSAP-QSYSSSSSSSGLTVPVQDLASIPEDPE 56
DB 28 SQSQGTSPQLHDLQYQGASSSTSTVPSSQSSSSSGLTSSLETSTQELCSIPEDQE 87
QY 57 IDEDIPQWGLWALGKGFNLHDCHEEYVGRKKDYTFDI PVNLQDRTYKTSKHF 116
DB 88 PEEFGPTPWAELWALQDGFNLDCVNDNYWGRDKSCYCFDGPLLKRDKYRTYSKHF 147
QY 117 RIFELGHGSRVANIENLNGTFFVKEIIGKRTPLTNNAEIALSLPTNKVFVFDL 176
DB 148 RIFREMGPKNYIYVLEHDSNGTFFVTEIELKGKRCPLNNSEIALSLCRNKVFVFDL 207
QY 177 SVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIIISKRKFKNMSSN- 235
DB 208 TVDQSVYPKELRDEYIMSKTGLSGACGEVKWAFERCKKVAIKIIISKRFPALGSSREA 267
QY 236 BHPISVDTEIELKLHPCIIKIENFPDSEDFYIYVLELMEGGELFDRVNVNSTRLREPI 295
DB 268 DTAPSVETEIELKLHPCIIKIENFPDSEDFYIYVLELMEGGELFDRVNVNKKELKAT 326
QY 296 AKLYFYQMLLAVQYLHENGVIHRDLKPNVLLSSTSECCIKITDFGQSKILGETSLMRT 355
DB 327 CKLYFYQMLLAVQYLHENGVIHRDLKPNVLLSQEEDCLIKITDFGQSKILGETSLMRT 386
QY 356 LCGTPTLYLAPEVLNTAGTGYSSAVDCWMSLVILFVCLGYPPESEQNSNPLKKNQ1ABG 415

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Db 387 LCSTPYLAPEVLISNGTAGSYRAVDCWSGLVFLICLSGYPPFSEHKQVSLQOITSG 446
QY 416 KYTYIAAAWNVSEQAFDLVKNLLVVDPEQRLTKQALEHPWLQDPSMKHITVERLMYGV 475
Db 447 KYNLPEVWTDVSEKALDLVKLLVVDPKARLTTEALSHPLQDEHMKKKFQDILLVQEK 506
QY 476 HTWPPPI--KXNLIIRKGHWDP--QDASTSS-----CSEIL 507
Db 507 NLVPLPLAPAQTSQGRKPLELEADAESSKRLAVCKRAVL 545

RESULT 5
CHK2_MOUSE
ID CHK2_MOUSE STANDARD; PRT; 546 AA.
AC Q92265;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serine/threonine-protein kinase Chk2 (EC 2.7.1.37).
GN Name=Chk2; Synonyms=CHK2, Rad53;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99055399; PubMed=9836640; DOI=10.1126/science.282.5395.1893;
RA Matsuo S., Huang M., Elledge S.J.;
RT "Linkage of ATM to cell cycle regulation by the Chk2 protein kinase.";
RL Science 282:1893-1897(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NMRI; TISSUE=Mammary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Controls cell cycle checkpoint. May participate in
transduction of the DNA damage and replicational stress signals.
CC Inhibits CDC25 phosphatase by phosphorylating it, preventing the
entry into mitosis. May have a role in meiosis as well.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- ENZYME REGULATION: Kinase activity is up-regulated by
autophosphorylation. Rapidly phosphorylated in response to DNA
damage and to replication block (By similarity).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CDS1
subfamily.
CC -!- SIMILARITY: Contains 1 FHA domain.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF086905; AAC83694.1; --
CC EMBL; BC056617; AAH56617.1; --
CC HSSP; OS6017; IGXC.
CC MGI; MGI:1355321; Chk2.
CC InterPro; IPR000253; FHA.
CC InterPro; IPR011009; Kinase like.
CC InterPro; IPR000719; Prot kinase.
CC InterPro; IPR008271; Ser Thr pkin_AS.
CC InterPro; IPR008984; SMAD_FHA.
CC Pfam; PF00498; FHA; 1.
CC Pfam; PF00069; Kinase; 1.
CC ProDom; PD000001; Prot kinase; 1.
CC PROSITE; PS00006; FHA DOMAIN; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; FALSE_NEG.
CC PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC KW ATP-binding; Cell cycle; Nuclear protein; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 117 179
FT NP_BIND 224 490
FT NP_BIND 230 238
FT BINDING 253 253
FT ACT_SITE 351 351
SQ SEQUENCE 546 AA; 61088 MW; A7949EFB5572CDA4 CRC64;

Query Match 60.4%; Score 1637; DB 1; Length 546;
Best Local Similarity 63.0%; Pred. No. 4.5e-96;
Matches 320; Conservative 71; Mismatches 107; Indels 10; Gaps 5;

QY 9 ESQQSQGTSSSSSSAP-OSYSQSSSSGTLSDITVPQDLASIPDDPIDEDIPQWGR 67
Db 40 ELSQYGGSSSSSTGTPSSSSQSSSSGTLSSLETSTVSTQELCSIPEDQPEEPGPAPAR 99
QY 68 LHALKGFNLHDLHHEHYVFGDKKDYTFDIPVLNQTDRTYKTYKRPRIPOELGHGHS 127
Db 100 LHALQDGFNLDCVNDYVFGDKSCYCFDGLLRRTDKYRTYSKKHFRIFREMGPKNC 159
QY 128 RVANTEDLSGNTGVNKEITIGKRTLPNTNNAEIALSLPTNKVFVFSDLSDVDOTIYPKD 187
Db 160 YIVYIEDHSGNGTFVNTLIGKGRCPSSNNSEIALSLCRNKVVFVFDLTVDDQSYVPKE 219
QY 188 FIDKYMSPISGACGEVKLAFQKSVCKKAVKIIKSKRKNMTSSN-EHPLSDVTEIE 246
Db 220 LRDEYIMSKTSGACGEVKMAFERKTCQVAKIISKRPALGSSREADTAPSVETEIE 279
QY 247 ILKLDHPICIIKENFFDSDFYIVLELMGEGELFDRVNVNSTRLEPIAKLYFYQMLA 306
Db 280 ILKLNHPICIIKIDVFDAD-YYIVLELMGEGELFDRVNVNKRLEATCKLYFYQMLA 338
QY 307 VOYLHENGVIHDLKPEVNLISSTSECCIKITDFGQSKILGETSLMRTLCTGPTVLAPE 366
Db 339 VOYLHENGVIHDLKPEVNLISSTSECCIKITDFGQSKILGETSLMRTLCTGPTVLAPE 398
QY 367 VLNTACTTGYSAVDCWSGLVFLICLSGYPPFSEKNSNIPKNAEGKYTYIAAARN 426
Db 399 VLVSNGTAGSYRAVDCWSGLVFLICLSGYPPFSEKTKQVSLKDQITSGKYNFPEVWD 458
QY 427 VSEQAFDLVKNLLVVDPEQRLTKQALEHPWLQDPSMKHITVERLMYGVDPH--TMPPEIKK 484
Db 459 VSEALDLVKLLVVDPKARLTTEALSHPLQDEYMKKKFQDILLVQEKNSVTLVPAPAQ 518
QY 485 NIIRKGHWDPDASTSS-----CSEIL 507
Db 519 TSSQKRPLEVEGMPSTKRLSVCGAVL 546

RESULT 6
Q6QAll
ID Q6QAll
AC Q6QAll;
PRT; 586 AA.
PRELIMINARY;

```



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Db 61 SSETVSTQELISIPEDQPEOEPEPTAPAPARLWALQDGFANDECVDNWFGRDKS 120
Qy 93 CDYTEDIPVNLQDRTYKTKRHFRIQELGHGHRVANIEDLSNGTGFVNKEIIGKGR 152
Db 121 CEYCFDEPLKRTDKYRTYKXKHFRIQELGHGHRVANIEDLSNGTGFVNKEIIGKGR 180
Qy 153 LPLTNNAETALSPTNKKVVFSDLSVDDQTIYKPKFIDKYMRSRPIGSGACGEVKLAF 212
Db 181 RPLNNNSEIALSLRNKVFVFDLTVDQSVYKALRDEYIMSKTLGSGACGEVKLAF 240
Qy 213 SVCKKVAVKIISKRFKMTSSNEHP- ISVDTEIELKKLDHPICIIKENFFDSDFYI 271
Db 241 KTKCKVAVKIISKRFKMTSSNEHP- ISVDTEIELKKLDHPICIIKENFFDSDFYI 299
Qy 272 VLEMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYHLHNGVHRDLKPNVLLSSTS 331
Db 300 VLEMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYHLHNGVHRDLKPNVLLSSTS 336
Qy 332 ESCCIIKITDFGOSKILGETSLMRTLCGTPTTYPYLAPEVNTAGTYSSAVDCWSLGVILFV 391
Db 337 -----ITDFGHSKILGETSLMRTLCGTPTTYPYLAPEVNTAGTYSSAVDCWSLGVILFV 390
Qy 392 CLCGVPPRSEQNSNIPKNOIAEGKYTYIAAARNVSEQAFDLVKNLAVVDPQRLTTKQ 451
Db 391 CLSGVPPRSEHRTQVSLKQDQISGKNFIPVMAEVSSEKALDLVKLLVVDPRKPTTEE 450
Qy 452 ALEHPWLQDSSMKHTVERLMYGVDMTPPP- IKNNIIRKKGHEWDQDASTSS- -C 503
Db 451 ALRHPWLQDSSMKHTVERLMYGVDMTPPP- IKNNIIRKKGHEWDQDASTSS- -C 503
Qy 504 SEIL 507
Db 511 AAVL 514

RESULT 8
Q902Y5 PRELIMINARY; PRT; 503 AA.
AC Q902Y5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein kinase Chk2.
GN ORFNames=zgc:55865;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA Chou C.-M., Liu J.-H., Huang C.-J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; AF265346; AAK52419.1; -.
DR HSSP; P49137; INXK.
DR ZFIN; ZDB-GENE-030131-8942; zgc:55865.
DR GO; GO:0005524; F-ATP binding; IEA.
DR GO; GO:0004674; F-protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50006; FHA DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 503 AA; 56699 MW; BC01BF3D84CEC71 CRC64;
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Query Match 48.6%; Score 1317.5; DB 2; Length 503;
Best Local Similarity 53.7%; Pred. No. 9.1e-76;
Matches 264; Conservative 86; Mismatches 125; Indels 17; Gaps 7;

Qy 3 SRDVTESQ-OSQSTSSSSSSSAPOSYSQ--SSSGTTLSSLDTPVQDLASIPEDPEIDE 59
Db 8 SGESOSQTSQTSOPASSSSSAPTSSSGSSSGSTLSSVDTPVQELQSPEDDE--E 65
Qy 60 DIPQWAGRLWALGKFLNHDCLHBEYVFRGRDKCYTTFDIPVLNQTDRTYKTKRHFRI 119
Db 66 VQPVQWAGRIIPLKQFQSVLNCNTENQYSGRDKRCDSYFSNSILKSPYNTYKSKHFRIF 125
Qy 120 QELGHGHRVANIEDLSNGTGFVNKEIIGKGRTLPLTNNAETALSPTNKKVVFSDLSVD 179
Db 126 RD-----ENLVLELDSNGTGFVNKEIIGKGRTLPLTNNAETALSPTNKKVVFSDLSVD 180
Qy 180 DOTIYPKDFIDKYIMRSRPIGSGACGEVKLAFKSVCKKVAVKIISKRF-KNNTSSNEHP 238
Db 181 DQANLPLEFSKYHARKITGVCGEVKLAIEKETFKKVALKTINKHDFPSIGTATR--- 237
Qy 239 ISVDTEIELKKLDHPICIIKENFFDSDFYIVLELMEGGELFDRVNVNSTRLEPIAKL 298
Db 238 -NAEREIELKKLDHPICIIKENFFDSDFYIVLELMEGGELFGRIRAKKKLEEDIACL 296
Qy 299 VFYQMLLAVQYHLHNGVHRDLKPNVLLSSTSBECCIKITDFGOSKILGETSLMRTLCG 358
Db 297 VFYQMLKAVEYHLNNGIHRDLKPNVLLSHADDICLIKITDFNQSKILEESLMKTLGC 356
Qy 359 TPTYLAPVNTAGTYSSAVDCWSLGVILFVCLGYPFPPSEONSNIPLKNOIAEGKYT 418
Db 357 TPTYVAPVFTASTVGTAKVDYWSLGVILFVCLGYPFPPSEONSNIPLKNOIAEGKYT 416
Qy 419 YIAAAWRNVSEQAFDLVKNLAVVDPQRLTTKQALEHPWLQDSSMKHTVERLMYGVDMTP 478
Db 417 FIPSQKNVSNKADLVKLLVVDQPKLSVEEALHHPWLKDRVRQNAQLMN--PGAA 474
Qy 479 PPPIKKNIRKR 490
Db 475 NQMPREPTRKR 486

RESULT 9
Q803E2 PRELIMINARY; PRT; 503 AA.
AC Q803E2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CHK2 checkpoint homolog.
GN ORFNames=zgc:55865;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=AB; TISSUE=whole body;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton G., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP	[2]
RN	SEQUENCE FROM N.A.
RC	STRAIN=AB; TISSUE=Whole body;
RA	Strausberg R.;
CC	-Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC	-1. SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR	EMBL; BC044519; AAH44519.1; -.
DR	HSSP; P49137; INXK.
DR	ZFIN; ZDB-GENE-030131-8942; zgc:55865.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR	GO; GO:0016740; F:transferase activity; IEA.
DR	GO; GO:0006468; F:protein amino acid phosphorylation; IEA.
DR	InterPro; IPR000253; FHA.
DR	InterPro; IPR011009; Kinase like.
DR	InterPro; IPR000719; Prot.kinase.
DR	InterPro; IPR002290; Ser_thr_kinase.
DR	InterPro; IPR008271; Ser_thr_pkin_AS.
DR	InterPro; IPR008984; SWAD_FHA.
DR	Pfam; PF00498; FHA; 1.
DR	Pfam; PF00069; Kinase; 1.
DR	ProDom; PD000001; Prot.kinase; 1.
DR	SMART; SM00240; FHA; 1; 1.
DR	SMART; SM00220; S_TRG; 1.
DR	PROSITE; PS50006; FHA DOMAIN; 1.
DR	PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ	SEQUENCE 503 AA; 56557 MW; 351A24EA58BAF8D5 CRC64;

Query Match 48.4%; Score 1311.5; DB 2; Length 503;
 Best Local Similarity 53.7%; Pred. No. 2.2e-75;
 Matches 264; Conservative 84; Mismatches 127; Indels 17; Gaps 7

Qy	3	SRDPKTSSQ-QSQGTSSSSSSASQSYSQ--SSSGTSLSSLDTPVQDLASIPEDPEIDE	59
Dd	8	SGESQSQTQSTQSQAPASSSSSASPSSSQGSQSGTLSSVDTPVQELQSIPEDEE--E	65
Qy	60	DIPQGWGRWLALGKGLNHDCLEHYEVYRGRKKCDYTEDIPLVNQTDKYTKYSKHFRIF	119
Dd	66	VQPQWGERTIPLKGFSVLNCTENQYSFGRRKCRDYSFNSILKKSPTFNYSKKGHRIF	125
Qy	120	QELGHGHSRVANIEDLSNGTGTFVNKEIIIGKRTLPFLTNNAIASLPTNKVFVSFLSDVSD	179
Dd	126	RD-----ENVLYLEDLSNGTWVDDEKLGNQGQSLGNNSVIALAEQKHQVFMFDKWAD	180
Qy	180	DOTYPKDFIDKYIMRSPIPGSAGCEVKLAQKSVCKKVAVKIISKRF-KNTSSNEHP	238
Dd	181	DQANLPLEFSKYYHARKIGTVGCVEVKLAIEKETFFKVALTKINKHDPPSIGTATR---	237
Qy	239	ISVTETEILKLDHPICIIKENPFDSDFYIVLELMEGEGLPDVRVNVNSTLRPEIAKL	298
Dd	238	NAREHEILKKIDHPCLUKTEDFYQTESDYIIVLEYIEGGELFGRIKAKKKLEEDIAKL	296
Qy	299	IFYQMLLAVQYLHENGVIHRDLKPENLVLLSSTSBECCKIKITDFGOSKITGETSLMRTLCG	358
Dd	297	IFYQMLKAVEYLNHNGIIHRDLKPENVLLASHDDICLIKITDFNQSKILESSLMKTLGG	356
Qy	359	TPTYLAPEVLNATGTTGYSSAVDCWSLGVLIVFCVLCGYPPSPSEQSNSNIPLKNOIAEGKYT	418
Dd	357	TPTYVAPEVFTASTVGTYTKADVMSLGVLLFICLGGYPPNFTECTTMSVREQINGEYR	416
Qy	419	YIAAARNVVSQAFLDVKNGLVVDPQEQLTTKQALEHPWLODDSMMKHTVERLMYGVDMTH	478
Dd	417	FIPQMRNVSNKAOLVKGLLVDPDQKRLSVEEALEHPWLDKDRVRQNANLMN--PGAA	474
Qy	479	PPPQQNIIRKR	490

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QY 332 EECIKITDFGQSKILGETSLMRTLCTPTYLAPVNLTAGTGYSSAVDCWLSGLVILFV 391
Db 269 EDCIKITDFGHSKILGETSLMRTLCTPTYLAPVNLVGTAGYNRAVDCWLSGLVILFI 328
QY 392 CLCGYPPFSSQNSNIPKLNQIAEGKITYIAAARNVSEQAFDLVKNLLVVDPQRLTTKQ 451
Db 329 CLSGYPPFSEHRTQVSLKQDITSGKYNFIPVWAEVSEKALDLVKKLLVDPKARFTTEE 398
QY 452 ALEHPWLQDSMKHTVERLMYGVHDHTMPPP---IKNNIRKRGHEWDQDASTSS-----C 503
Db 389 ALRHPWLQDDMKRKTQDLLSEENESTALPQVLAQPSRKRPREGEAEGAEITTKRPVAVC 448
QY 504 SEIL 507
Db 449 AAVL 452

RESULT 11
Q9HBS5
ID Q9HBS5 PRELIMINARY; PRT; 322 AA.
AC Q9HBS5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,
RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,
RA Yu J., Han L.H.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; A217975; AAG17218.1; -.
DR HSSP; P49137; INXK.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot.kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR ProDom; PD000001; Prot.kinase; 1.
DR SMART; SM00220; S_TKC_1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Hypothetical protein; Kinase;
KW Serine/threonine protein kinase; Transferase.
KW SEQUENCE 322 AA; 36157 MW; D31257F4B9652438 CRC64;

Query Match 39.3%; Score 1066; DB 2; Length 322;
Best Local Similarity 63.8%; Pred. No. 5.4e-60;
Matches 206; Conservative 44; Mismatches 63; Indels 10; Gaps 4;

QY 194 MSRPISGAGGEVKLAFQSVCKKAVKIISKKEKMTSSNEHP-LSVDTEIILKKLD 252
Db 1 MSKTLGSGAGGEVKLAFQSVCKKAVKIISKRRFAIGSAREADPALNVETEILDKLN 60
QY 253 HPCIIEKNFFDSEDFYIIVLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVOYLHE 312
Db 61 HPCIIEKNFFDAED--YIIVLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVOYLHE 119
QY 313 NGVIHRLDPENVLLSSTSECCIKITDFGQSKILGETSLMRTLCTPTYLAPVNLTAG 372
Db 120 NGIHRDLDPENVLLSQBEDCLIKITDFGHSKILGETSLMRTLCTPTYLAPVNLVSVG 179
QY 373 TTGYSSAVDCWLSGLVILFCLCGYPPFSSQNSNIPKLNQIAEGKITYIAAARNVSEQAF 432
Db 180 TAGYNRAVDCWLSGLVILFCLSGYPPFSEHRTQVSLKQDITSGKYNFIPVWAEVSEKAL 239
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QY 433 DLVKNLLVDPQRLTTKQALEHPWLQDSMKHTVERLMYGVHDHTMPPP---IKNNIRK 489
Db 240 DLVKNLLVDPQRLTTKQALEHPWLQDSMKHTVERLMYGVHDHTMPPP---IKNNIRK 299
QY 490 RGHEWDQDASTSS-----CSEIL 507
Db 300 RPREGEAEGAEITTKRPVAVCAAVL 322

RESULT 12
Q6QA08
ID Q6QA08 PRELIMINARY; PRT; 339 AA.
AC Q6QA08;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein kinase Chk2 transcript variant del9-12.
GN Name=CHK2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Breast carcinoma;
RA Staalesen V., Falck J., Geisler S., Bartkova J., Borresen-Dale A.-L.,
RA Lukas J., Lillehaug J.R., Lonning P.E.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY551300; AAS58461.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000253; FHA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot.kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR008984; SMAD_FHA.
DR Pfam; PF00498; FHA; 1.
DR ProDom; PD000001; Prot.kinase; 1.
DR SMART; SM00240; FHA; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS50006; FHA_DOMAIN; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW Kinase.
KW SEQUENCE 339 AA; 38125 MW; CAE0E59DF0308393 CRC64;

Query Match 37.3%; Score 1012.5; DB 2; Length 339;
Best Local Similarity 60.2%; Pred. No. 1.5e-56;
Matches 203; Conservative 47; Mismatches 56; Indels 31; Gaps 5;

QY 2 MSRDITKTESQ-----QSQGTSSSSSSSNAP-QSYQSSSSSGTL 37
Db 1 MSRESDEVAQSQSHGSSACSQPHGSVTQSGSSSQSGISSSTSTWPNSSSHSSGTL 60
QY 38 SSLDTPVPQDLASI-----PEDEIDEDIPQWGRWLWALGKGLNHDCLHEEVVFGDRKK 92
Db 61 SLEIVTSVQELYSIPEDQEPEDQEEPTFPAPARLWALQDGFANLECVNDYWFGRDKS 120
QY 93 CDYTFDIPVLNQTDRYKYSKHFRIFOELGHGHSRVANIEDLSNGNTPFNKEIIQKGR 152
Db 121 CEYCFDEPLLRKTRTYYSKKHFRIFREVGPKNSYIAVEDHSGNGTFTVNTLVGKGR 180
QY 153 LPLTNNAETLSLPNKKVVFSDLSVDDQTIYPKDFIDKYINSRPIGSGACGEVKLAFQK 212
Db 181 RPLANNSETLSLRNKKVVFDFDLTVDDQSVYPKALRDEYIMSKTLGSGACGEVKLAF 240
QY 213 SVCKKAVAKIISKRRFKMTSSNEHP-LSVDTEIILKKLDHPCIIEKNFFDSEDFYI 271
Db 241 KYCKKVAIKIISKRRFAIGSAREADPALNVETEILKKLNHPCIIEKNFFDAED--YI 299
QY 272 VLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQ 308
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InterPro: IPR008984; SMAD_FHA.
PFam: PF00498; FHA; 1.
PFam: PF00069; Pkinase; 1.
ProDom: PD000001; Prot_kinase; 1.
SMART: SM00240; FHA; 1.
SMART: SM00220; S_TK; 1.
PROSITE: PS00067; FHA DOMAIN; 1.
PROSITE: PS00107; PROTEIN KINASE ATP; 1.
PROSITE: PS00111; PROTEIN KINASE DOM; 1.
PROSITE: PS00108; PROTEIN KINASE_ST; 1.
Alternative splicing: ATP-binding; Nuclear protein;
Serine/threonine-protein kinase; Transferase.
FT DOMAIN 69 129
FT 174 441
FT NP BIND 180 188
FT BINDING 203 203
FT ACT SITE 303 303
FT VARSPIC 46 62
FT /FTID=VSP_004865.
SQ SEQUENCE 476 AA; 54261 MW; 58D583E015C4B626 CRC64;
Query Match 30.5%; Score 828; DB 1; Length 476;
Best Local Similarity 36.8%; Pred. No. 1.3e-44;
Matches 190; Conservative 90; Mismatches 162; Indels 74; Gaps 13;
QY 2 MSRDYKTESQSQSGTSSSSSSAPOSYSQSSSGTSLSSLDTPVPQDLASIPEDPEIDEDI 61
DB 1 MARDT---QGTQGT-----QSQASNIWTQVESQPEKIV----- 31
QY 62 PQPWGLWALGKGF-----LNHDCLEHYEYVGRDKKCDYTF-----DI 99
DB 32 ---WGLY--GRNIIKISLTSKYRIIYTHSSFSVDLNDEFTAGRGEANDLILTLNDL 86
QY 100 P--VLNQTDRYKTYSKRHFRIPOELGHGHSRVANIEDLSGNGTFVFNKEIIGKGRTLPLTN 157
DB 87 PEKILTR-----ISKVHF-IIRKANCELTNPVYIQDLSRNGTFVFNKEIGTNRMLKN 139
QY 158 NABEIALSLPTNKVFPSDLSDVDDQTYIPKDFIDKYMISRPISGSGACGEVKLAFQSKYCKK 217
DB 140 DDVLSLSHTPYKAFVFKDLSPNESIGLPEEINKTYVNRKLGSGAYGLVRLVYDTRTCQQ 199
QY 218 VAVKIISKRFK-MNTSSN-EHPISVDTEIELKLHPICLIKENFDSDFYIVVLEL 275
DB 200 FAKMIYKKQMLSGARPTNFSFDPDRVLNEAKIMKMLSHPCVVRMHDIYDKPDSYVMYLEF 259
QY 276 MEGGELFDRVNSTRLREPIAKLYFVOMLAVOYLHENGTVHRLKPEVLLSTSECC 335
DB 260 MRGGDLNRIISKNLSEDISKLYFYQCHAVKYLHDRGITHRLKPDNVLLETNDSETL 319
QY 336 IKITDFGSKILGETSLMRTLCTGTPYLAPEVINTAGTGYSSAVDVCWSLGVILFVCLG 395
DB 320 LKVSDFGLSKFVKQDSWMTLCTGTPYLAPEVILTGREATKKVDIWSLGVILFVCLSG 379
QY 396 YPPFSQSNIPILNQIAGKYTYIAAARNVSEQAFLVKNLLVDPPEQRLLTYKQALEH 455
DB 380 TLPFSDEYGT-PAAQOIKKGREAYGHPWSKVSQRAKLINQMLIVDPERRPSIDDLVQS 438
QY 456 PWLQDSMKHTVERLM-----YGVDTHTWPPPIKEN 485
DB 439 SWLRDAPMLQAKRLMKLGMIEBENFLEPPTKRS 474
RESULT 14
Q6QA10 PRELIMINARY; PRT; 289 AA.
AC Q6QA10;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Protein kinase Chk2 transcript variant del7.
GN Name=CHK2;
OC Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RA Staalesen V., Falck J., Geisler S., Bartkova J., Borresen-Dale A.-L.,
RA Lukas J., Lillehaug J.R., Lonning P.E.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY551298; AAS58459.1; -;
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; P:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR00253; FHA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR00719; Prot_kinase.
DR InterPro; IPR008984; SMAD_FHA.
DR Pfam; PF00498; FHA; 1.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00240; FHA; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00107; Pkinase.
KW Kinase.
SQ SEQUENCE 289 AA; 32141 MW; 630D0AF3AE5114B6 CRC64;
Query Match 29.2%; Score 791; DB 2; Length 289;
Best Local Similarity 56.4%; Pred. No. 1.6e-42;
Matches 159; Conservative 42; Mismatches 51; Indels 30; Gaps 4;
QY 2 MSRDYKTESQ-----QSQGTSSSSSSAP-QSYSQSSSSGTL 37
DB 1 MSRESDEVAQOQSHGSSSACSQPHGQSVTQSGSSSQSQGISSTSTWPNSSQSSSHSSGTL 60
QY 38 SLSLTPVPQDLASI-----PEDPEIDEDIPOWGLWALGKGLNHDCLHEEYVGRDKK 92
DB 61 SSLETVTQELYSIPEQEPEDPEPTAPWRLWALQOQGANLECVNDNVYFGRDKS 120
QY 93 CDYTPEDIPLNQTDRYKTYSKRHFRIPOELGHGHSRVANIEDLSGNGTFVFNKEIIGKGR 152
DB 121 CEYCFDEPLLKRTDKYTSKKHFRIFREVGPKNYSIAYIEDHSGNGTFVNTLVGKGR 180
QY 153 LPTNABEIALSLPTNKVFPSDLSDVDDQTYIPKDFIDKYMISRPISGSGACGEVKLAFQK 212
DB 181 RPLANNSEIALSLRNKVFVFDLTVDQSVYPKALRDEYIMSKTLGSGACGEVKLAF 240
QY 213 SVCKKVAVKIISKRFKKNWTSNEHP-ISVDTEIELKLKH 253
DB 241 KTCRKVAIKIISKRFKAIGSAREADPALNVETEIELKLKH 282
RESULT 15
Q7SEK0 PRELIMINARY; PRT; 712 AA.
AC Q7SEK0;
DT 01-NAR-2004 (TrEMBLrel. 26, Created)
DT 01-NAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-NAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU02814.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehan B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothke G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,

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OM protein - protein search, using sw model

Run on: July 7, 2005, 12:33:18 ; Search time 162 Seconds
(without alignments)
1234.291 Million cell updates/sec

Title: US-10-618-173-2

Perfect score: 2712

Sequence: 1 MMSRDTKTESQSQSGTSSSS.....ASTSSCSILPTSAEKRAKR 517

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003Bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2712	100.0	517	5 AAB47789	Aab47789 Protein k
2	1656	61.1	542	4 AAG68375	Aag68375 Human Chk
3	1655.5	61.0	543	2 AAY06204	Aay06204 Human che
4	1655.5	61.0	543	2 AAY05765	Aay05765 Novel hum
5	1655.5	61.0	543	5 AAM48995	Aam48995 Human Chk
6	1655.5	61.0	543	5 AAG30701	Abg30701 Human che
7	1655.5	61.0	543	8 ADL32561	Adl32561 Human Chk
8	1655.5	61.0	543	8 ADM72213	Adm72213 Human TAS
9	1655.5	61.0	543	8 ADO44010	Ado44010 Amino aci
10	1655.5	61.0	543	8 ADQ09232	Adq09232 Human CHE
11	1651.5	60.9	543	5 AAM48996	Aam48996 Human Chk
12	1643.5	60.6	543	3 AAY67968	Aay67968 Human cel
13	1624	59.9	586	8 ADM61455	Adm61455 Human KPP
14	1499	55.3	514	8 AAM48994	Aam48994 Human Chk
15	1499	55.3	514	8 ADL32563	Adl32563 Human Chk
16	838.5	30.9	459	4 ABB65298	Abb65298 Drosophil
17	621	22.9	513	8 ADN18925	Adn18925 Bacterial
18	603	22.2	356	4 AAB84360	Aab84360 Amino aci
19	600.5	22.1	355	4 AAB50055	Aab50055 Murine de
20	600.5	22.1	355	4 AAE11777	Aae11777 Human kin
21	600.5	22.1	355	5 AAM41268	Aam41268 Human pol
22	600.5	22.1	355	5 ABB08178	Abb08178 Human Cam
23	600.5	22.1	357	4 AAE11768	Aae11768 Human kin
24	600.5	22.1	357	8 ADJ75440	Adj75440 Marker ge
25	600.5	22.1	357	8 ADQ15044	Adq15044 Human can

ALIGNMENTS

RESULT 1

AAB47789

ID AAB47789 standard; protein; 517 AA.

XX

AC AAB47789;

XX

DT 04-MAR-2002 (first entry)

XX

DE Protein kinase Cds1.

XX

KW Protein kinase; Xenopus; Cds1; Xcds1; DNA damage checkpoint; cell cycle; Cdc25; forkhead-associated domain; FHA domain; ATM; ATR; DNK-PK; Chk2; human; mitotic delay.

XX

OS Xenopus laevis.

XX

PN WO200183703-A2.

XX

PD 08-NOV-2001.

XX

PF 04-MAY-2001; 2001WO-US014646.

XX

PR 04-MAY-2000; 2000US-0202028P.

XX

PA (CALY) CALIFORNIA INST OF TECHNOLOGY.

XX

PI Dumphy WG, Guo Z;

XX

DR WPI: 2002-066528/09.

XX

DR N-PSDB; AAI72072.

XX

PT Novel polypeptide for regulating cell cycle progression, which is activated and phosphorylated in response to double-stranded DNA useful for diagnosing and treating cell proliferative disorder.

XX

PS Claim 2; Fig 2; 75pp; English.

XX

CC This sequence shows the protein kinase, Xenopus Cds1 (Xcds1) which plays a role in DNA damage checkpoint and regulating progression of cell cycle. The protein is characterized as phosphorylating Cdc25 or its homolog, having a molecular mass of 58 kD, 517 amino acids, SQ/TQ motifs at the amino terminal region, a carboxyl terminal kinase domain and an amino terminal forkhead-associated (FHA) domain. Xcds1 phosphorylates Cdc25 on Ser287 in the 14-3-3 binding site, which inhibits its activity. Xcds1 is activated by poly(dT)40. When Xcds1 is phosphorylated in extracts containing poly(dT)40, hyperphosphorylated Cds1 shows a five- to six-fold increase over background in its kinase activity towards GST-cdc25[254-316]-WT. The SQ/TQ motifs at the amino terminal end of Xcds1 are

CC potential substrates for kinases such as ATM, ATR and DNK-PK that are
CC involved in checkpoint pathways. The C-terminal kinase domain is the most
CC conserved region of Xcd1 when compared to Chk2, the human homologue of
CC Xcd1. Cdel protein or mRNA is useful for diagnosing a Cdel-associated
CC disorder in a subject, by determining the level of Cdel mRNA or protein
CC expression in the subject, where a low level of Cdel in the subject
CC compared to a control is indicative of a Cdel-associated disorder.
CC Oligonucleotides (see A172073-75) which form double stranded regions
CC with Xcds DNA are useful for increasing mitotic delay in a vertebrate
CC cell

XX
SQ Sequence 517 AA;
Query Match 100.0%; Score 2712; DB 5; Length 517;
Best Local Similarity 100.0%; Pred. No. 8e-248;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSRDTKTESQSQSGTSSSSSSAPQSYSSQSSSGTSSLDTPVPQDLASIPEDPEIDED 60
DB |||||
QY 1 MMSRDTKTESQSQSGTSSSSSSAPQSYSSQSSSGTSSLDTPVPQDLASIPEDPEIDED 60
DB |||||
QY 61 IPQPGRLWALGKFLNHDCLHEEYVFGDKKCDYTFDIPVLNQTDRKTYSKRHFRIQ 120
DB |||||
QY 61 IPQPGRLWALGKFLNHDCLHEEYVFGDKKCDYTFDIPVLNQTDRKTYSKRHFRIQ 120
DB |||||
QY 121 ELGCHGHSRVANTEDLSGNGTFFVKNELIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
DB |||||
QY 121 ELGCHGHSRVANTEDLSGNGTFFVKNELIIGKGRTPLTNNAEIALSLPTNKVFVFSLSVDD 180
DB |||||
QY 181 QTIYPKDFIDKYMIRPIGSGAGCEVKLAFQSKVCKKAVAKIIISKRKFQMTSSNEHPIS 240
DB |||||
QY 181 QTIYPKDFIDKYMIRPIGSGAGCEVKLAFQSKVCKKAVAKIIISKRKFQMTSSNEHPIS 240
DB |||||
QY 241 VDETEILKLDHPICIIKIENFDSEDFYIIVLELMEGGELEFDRVNSTRLREPIAKLYF 300
DB |||||
QY 241 VDETEILKLDHPICIIKIENFDSEDFYIIVLELMEGGELEFDRVNSTRLREPIAKLYF 300
DB |||||
QY 301 YQMLLAVQYLHENGVIHRLDKPENVLSSSTSECCIKITDFGOSKILGETSLMRTLCTGP 360
DB |||||
QY 301 YQMLLAVQYLHENGVIHRLDKPENVLSSSTSECCIKITDFGOSKILGETSLMRTLCTGP 360
DB |||||
QY 361 TYLAPEVLNTAGTTGYSSAVDCMSLGVILFVCLCGYPPFSEQNSNIPLNQIAEGKYTI 420
DB |||||
QY 361 TYLAPEVLNTAGTTGYSSAVDCMSLGVILFVCLCGYPPFSEQNSNIPLNQIAEGKYTI 420
DB |||||
QY 421 AAARNVSEQAFDLVKNLLVDPPEQLTTKQALEHPWLQDDSMKHTVERLMYGVDDHTMPP 480
DB |||||
QY 421 AAARNVSEQAFDLVKNLLVDPPEQLTTKQALEHPWLQDDSMKHTVERLMYGVDDHTMPP 480
DB |||||
QY 481 PIKQNIIRKRGHEWDQDASTSSCSEILPTSAKRAKR 517
DB |||||
QY 481 PIKQNIIRKRGHEWDQDASTSSCSEILPTSAKRAKR 517
DB |||||

RESULT 2
AAG68375
ID AAG68375 standard; protein; 542 AA.
XX
AC AAG68375;
XX
XX
DT 13-JUL-2001 (first entry)
XX
DE Human Chk2 kinase protein sequence.
XX
KW Human; Cdc25C; Chk1; Chk2; G2 checkpoint; cell cycle regulation; cancer;
KW cell proliferation; apoptosis.
XX
OS Homo sapiens.
XX
PN WO200121771-A2.
XX
PD 29-MAR-2001.
XX

PF 21-SEP-2000; 2000WO-IB001438.
XX
PR 22-SEP-1999; 99JP-00269398.
PR 30-NOV-1999; 99JP-00340322.
XX
PA (CANB-) CANBAS CO LTD.
XX
PI Suganuma M, Kawabe T;
XX
XX WPI; 2001-343125/36.
DR
XX
XX
PT Isolated or recombinant polypeptide of 7-11 amino acids, useful for
PT treating cell proliferative disorders, e.g. to stop the growth of, or
PT kill cancer cells, by disrupting the G2 cell cycle arrest checkpoint.
XX
PS Disclosure; Page 26; 126pp; English.

XX
CC The present invention describes a number of peptides which disrupt the G2
CC cell cycle checkpoint when administered to a cell. They act by inhibiting
CC Chk2 (the sequence of which is shown here) and Chk1 kinases, and may be
CC derived from Cdc25C. The peptides are useful in the treatment of cell
CC proliferation diseases, such as cancer, as the inhibition of the Chks
CC allows DNA damage and induces apoptosis
XX
SQ Sequence 542 AA;

Query Match 61.1%; Score 1656; DB 4; Length 542;
Best Local Similarity 60.0%; Pred. No. 1.4e-147;
Matches 326; Conservative 74; Mismatches 105; Indels 38; Gaps 7;

QY 2 MSRDTKTESQSQSGTSSSSSSAPQSGSVTQSGSSSQSGISSSTSPNSQSSSSGTL 38
DB |||||
QY 1 MSRESDEVAQSHGSSACSPHGSVTQSGSSSQSGISSSTSPNSQSSSSGTL 60
DB |||||
QY 39 SLDTVPVQDLASIPEDPEIDEDIPQPGRLWALGKFLNHDCLHEEYVFGDRKK 93
DB |||||
QY 61 SLETVSTQELYSIPEDQEPDEPEPTAPARLWALQDGFANLECVNDNTWFGDRKSC 120
DB |||||
QY 94 DYTEDIPLVNTQDRKTYSKRHFRIFOELGHGHSRVANTEDLSGNGTFFVKNELIIGKGR 153
DB |||||
QY 121 EYCFDEPLKRTDKRTYTSKKHFRIFREVGPNYSYIYIEDHSGNGTFFVNTLGVKGR 180
DB |||||
QY 154 PLTNNAEIALSLPTNKVFVFSLSVDDQTIYPKDFIDKYMIRPIGSGAGCEVKLAFQKS 213
DB |||||
QY 181 PLNNSEIALSLRNKVFVFFDLTVDDQSVYFKALRDEYIMSKTLGSGAGCEVKLAFERK 240
DB |||||
QY 214 VCKKVAVKIIISKRKFQMTSSNEHP- ISVDTEILKLDHPICIIKIENFDSEDFYIIV 272
DB |||||
QY 241 TCKKVAIKIIISKRKFAIGSAREADPALNVETEILKLNHPCTIIKKNFDEAD-YIIV 299
DB |||||
QY 273 LELMEGGELEFDRVNSTRLREPIAKLYFQMLLAVQYLHENGVIHRLDKPENVLSSSTSE 332
DB |||||
QY 300 LELMEGGELEFDRVGNKRLKEATCKLYFQMLLAVQYLHENGVIHRLDKPENVLSSQEE 359
DB |||||
QY 333 ECCIKITDFGOSKILGETSLMRTLCTGPTTYLAPEVLNTAGTTGYSSAVDCMSLGVILFVC 392
DB |||||
QY 360 DCLIKITDFGHSKILGETSLMRTLCTGPTTYLAPEVLVSVGTAGYNRAVDCMSLGVILFIC 419
DB |||||
QY 393 LCGYPPFSEQNSNIPLNQIAEGKYTIYAAARNVSEQAFDLVKNLLVDPPEQLTTKQ 452
DB |||||
QY 420 LSGYPPFSEHRTQVSLKQDITSGKYNFIPVNAEYSEKALDLVKKLLVDPPEKARFTTEA 479
DB |||||
QY 453 LEHPWLQDDSMKHTVERLMYGVDDHTMPPP---IKQNIIRKRGHEWDQDASTSS---CS 504
DB |||||
QY 480 LHPWLQDDMKRKFQDLSEENESTALPQVLAQPSSTSRKPREGEAETTKRPAVCA 539
DB |||||
QY 505 EIL 507
DB :
DB 540 AVL 542

RESULT 3
AAY06204

ID AAY06204 standard; protein; 543 AA.
 AC AAY06204;
 XX
 DT 16-AUG-1999 (first entry)
 XX
 DE Human checkpoint kinase hCDS1.
 XX
 KW Checkpoint kinase; hCDS1; human; DNA damage; proliferative disease;
 KW cancer; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9925843-A2.
 XX
 PD 27-MAY-1999.
 XX
 PF 21-OCT-1998; 98WO-EP006981.
 XX
 PR 22-OCT-1997; 97GB-00022320.
 XX
 PA (SCRI) SCRIPPS RES INST.
 PA (JANC) JANSSEN PHARM NV.
 XX
 PI Luyten WHML, Parker AE, Megowan C, Blasina A;
 XX
 DR WPI; 1999-338010/28.
 DR N-PSDB; AAX58793.
 XX
 XX New human kinase used for treatment of cancer and proliferative diseases.
 XX
 PS Claim 9; Fig 2; 39pp; English.
 XX
 CC The present sequence represents a novel human checkpoint kinase, termed
 CC hCDS1, that acts in coordination with Cdc25 in the DNA damage checkpoint.
 CC The sequence is predicted from a cDNA (see AAX58793) isolated from a SK-N
 CC-MC neuroblastoma cDNA library. The predicted protein is 28% identical to
 CC the cdc1 protein of *S. pombe*. A 2.2 kb transcript is expressed in testis
 CC and in 8 human cancer samples examined. hCDS1, its inhibitors and
 CC activators, are useful for treating cancer or proliferative disease
 CC (claimed). Inhibitors and activators of the kinase activity can also be
 CC used in anti-cancer therapy, particularly by increasing susceptibility of
 CC cancer cells to chemotherapy and/or radiotherapy (claimed). hCDS1 is
 CC useful for modifying DNA damage checkpoint activity of a cancer cell
 CC (claimed)
 XX
 SQ Sequence 543 AA;
 Query Match 61.0%; Score 1655.5; DB 2; Length 543;
 Best Local Similarity 59.9%; Pred. No. 1.6e-147;
 Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
 QY 2 MSRDVTQESQ-----QSQGTSSSSSSAP-OSYSSSSGTL 37
 DB 1 MRRESVEAQSHGSSACSPHGSVTSQSSSSQSGISSSSTSTPNSSQSHSSGTL 60
 QY 38 SLDTPVQDLASI-----PEDPEIDEDIPQPMGRWLWALGKFLNHDCLHEEYVFGDRKK 92
 DB 61 SSLETSTQELYSIPEDQEPDQEPPEPTAPARLWALQDGFANLECYNDNTWFGDRKS 120
 QY 93 CDYTFDIPVLNQDRYTKYKHFRIQELGHGHSRVANIEDLSNGTTFVNEIKGRT 152
 DB 121 CEYCFDEPLLKRTYKRTYSKKHFRIFREVGPKNSYIAVIEDHSGNGTTFVNTLVGKGR 180
 QY 153 LPLTNAETALSPLTNKVFVPSDLSDVDOTIYKDFIKVMSRPIGSGACGEVLAFOK 212
 DB 181 RPLNNSEALSLSRKNVFFVFDLTVDQSVFPAURDETYSKTLGSGACGEVLAFAER 240
 QY 213 SVCKVAVKIISKRFKMTNSNEHP-ISYDTEILKLDHPCTIKIENFFDSEDFYII 271
 DB 241 KTCKVAIKIISKRFKAIGSAREADPALNVETIEILKLNHPCTIKIKNFDAED-YII 299
 QY 272 VLELMGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPENVLSSTS 331

Db 300 VLELMGGELFDKVVGNKELKEATCKLYFYQMLLAVQYLHENGVIHRDLKPENVLSSOE 359
 QY 332 EECCKITDFGOSKILGETSLMRTLCGTPTYLAPEVLNAGTGYSSAVDCWSLGVILFV 391
 Db 360 EDCLIKITDFGSHKILGETSLMRTLCGTPTYLAPEVLNAGTGYSSAVDCWSLGVILFI 419
 QY 392 CLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAFDLVRNLLVVDPEQRLLTKQ 451
 Db 420 CLSGYPPFSEHRTQVSLKQITSGKYNFTPEVMAEVSERKALDLVKKLLVVDPKARFTTEE 479
 QY 452 ALEHPWLQDDSMKHTVERLMYGVHDHTMPP-----IKGNIIRKRGHEWDQDASTSS-----C 503
 Db 480 ALRHPWLQDEDMKRFQDILLSEENSTALPQVLAQPSRKRPREGEASGAETTKRPAVC 539
 QY 504 SEIL 507
 Db 540 AAVL 543
 RESULT 4
 AAY05765
 ID AAY05765 standard; protein; 543 AA.
 XX
 AC AAY05765;
 XX
 DT 02-AUG-1999 (first entry)
 XX
 DE Novel human checkpoint kinase hCDS1.
 XX
 KW Cell cycle checkpoint kinase; human; hCDS1; cell proliferation; cancer;
 KW therapy; chemotherapy; adjunct.
 XX
 OS Homo sapiens.
 XX
 PN WO9920747-A2.
 XX
 PD 29-APR-1999.
 XX
 PF 21-OCT-1998; 98WO-EP006982.
 XX
 PR 22-OCT-1997; 97GB-00022320.
 XX
 PA (JANC) JANSSEN PHARM NV.
 XX
 PI Luyten WHML, Parker AE;
 XX
 DR WPI; 1999-288300/24.
 DR N-PSDB; AAX25464.
 XX
 XX Novel human cell cycle checkpoint kinase hCDS1, useful for treating cell
 XX proliferation diseases, e.g. cancer.
 XX
 PS Claim 2; Page 33-34; 35pp; English.
 XX
 CC The present sequence represents hCDS1, a novel human cell cycle
 CC checkpoint kinase that acts in coordination with Cdc25 at the DNA damage
 CC checkpoint, rather than the replication checkpoint as found in yeast. The
 CC hCDS1 sequence was predicted from hCDS1 cDNA (see AAX25464) that was
 CC obtained from a human SK-N-MC neuroblastoma cDNA library. It shows 28%
 CC identity with cdc1 protein of *S. pombe*, 28% identity to RAD53 and 27%
 CC identity to the DUN1 kinase of *S. cerevisiae*. Northern blot analysis
 CC identified a single transcript of about 2.2 kb expressed in testis and in
 CC 8 human cancer samples examined. The characterization of hCDS1 and the
 CC elucidation of its role in the DNA damage checkpoint allows for the
 CC preparation of pharmaceuticals and therapeutic methods for acting as an
 CC adjunct to chemotherapy of cancer. Thus, pharmaceutical formulations
 CC incorporating hCDS1 cDNA, RNA, antisense molecules, hCDS1 protein,
 CC antibodies against the protein, or other therapeutics identified in
 CC assays of the invention, can be administered in conjunction with any
 CC suitable chemotherapy agent to act as an adjunct to the main action of
 CC the chemotherapy agent

CC elevated expression of EDD protein in a cell; (11) an antisense nucleic acid, ribozyme, peptide nucleic acid (PNA), interfering RNA or siRNA; and (12) a pharmaceutical composition comprising the antisense nucleic acid, ribozyme, PNA, interfering RNA or siRNA. EDD has cytostatic activity, and can be used in gene therapy. The methods and modulator are useful for treating a condition associated with EDD over expression such as cancer, e.g. squamous cell carcinoma, hepatocellular carcinoma, ovarian cancer, breast cancer, melanoma, head and neck cancer, adenocarcinoma, squamous lung cancer, gastrointestinal cancer (e.g. gastric, colon, or pancreatic cancer), renal cell cancer, bladder cancer, prostate cancer, non-squamous carcinoma, glioblastoma and medullablastoma. The components and composition are useful for reducing the expression of EDD in a cell to inhibit cellular proliferation. The present sequence represents human Chk2 transcript variant 1 protein, which is used in the exemplification of the present invention.

XX Sequence 543 AA;

Query Match 61.0%; Score 1655.5; DB 8; Length 543;
Best Local Similarity 59.9%; Pred. No. 1.6e-147;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTSQ-----OSQGTSSSSSSAP-QSYSSSSSSTL 37
DB 1 MSRESDEAQQSHGSSACSPHGSVTSQSGSSSQSGISSSTSTMPNSSQSSHSSTL 60
QY 38 SSLDTPVQDLASI-----PEDPEIDEDIPQWGLMALGKFLNHDCLHEEYVGRDKK 92
DB 61 SSLETVSTQELYSIPEDQEPEDQEPPTAPWALMALQDGFANLECVNDNYWGRDKS 120
QY 93 CDYTFDIPVLNQTRYKTSKRHFRIFOELGHGHSRVANIEDLSGNGTFVFNKEIIGKRT 152
DB 121 CEYCFDEPLLKRTDKYRTSKKHFRIFREVGPKNSYIAYIEDHSGNGTFVNTLVGKGR 180
QY 153 LPLTNNAIALSLPNKVFVPSDLSDVDQTYPKDFIDKYIMSRPIGSGAGEVKLAFQK 212
DB 181 RPLNNSBIALSLSRNKVFVFDLTVDQSVYPKALRDEYIMSKTLGSGAGEVKLAFER 240
QY 213 SVCKKVAVKIISKRFKNTSSNEHP-ISVDTEIEILKLDHPCTIIKIENFDSDFYI 271
DB 241 KTCCKVAIKIISKRFKAIGSAREADPALNVETEIEILKLNHPCTIIKKNFDDAED-YII 299
QY 272 VLELMEGGELPDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPEENVLLSST 331
DB 300 VLELMEGGELPDKVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPEENVLLSQE 359
QY 332 BECCIKITDFGSKILGETSLMRTLCTGPTYLAPEVLNAGTGTGYSSAVDCWSLGVILFV 391
DB 360 EDCLIKITDFGHSKILGETSLMRTLCTGPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419
QY 392 CLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAFLVKNLLAVDPQRLTTKQ 451
DB 420 CLSGYPPFSEHRTQVSLKDKQITSGKYNFIPEVMAEVSSEKALDLVKLLVDPKARFTTEE 479
QY 452 ALEHPWLQDQSMKHTVVERIMYGVDRHTMPPP---IKKNIIRKRGHWDDQASTSS-----C 503
DB 480 ALRHPWLQDEDMKRFQDLSEENESTALPQVLAQPSISRKREPREGEAEGATTKRPVAVC 539
QY 504 SEIL 507
DB 540 AAVL 543

RESULT 8

ADM72213

ID ADM72213 standard; protein; 543 AA.

XX

AC ADM72213;

XX 17-JUN-2004 (first entry)

XX Human TASK108 polypeptide.

DE

XX

KW TASK; tumour-associated kinase; cytostatic; tumour antigen;
XX cell proliferative disorder; cancer; transgenic; human.

OS Homo sapiens.

PN WO2004024064-A2.

XX 25-MAR-2004.

XX 05-SEP-2003; 2003WO-US027894.

XX 11-SEP-2002; 2002US-0410166P.

XX (GETH) GENENTECH INC.

XX Desauvage FJ, Wood WI, Zhang Z;

XX WPI; 2004-282985/26.

XX N-PSDB; ADM72212.

PT New tumor-associated kinase nucleic acids and polypeptides, useful as
XX hybridization probes for isolating full length TASK DNA, for generating
XX transgenic animals, in chromosome identification, or for tissue typing.
XX Claim 12; SEQ ID NO 18; 163pp; English.

XX The invention relates to new isolated tumour-associated kinase (TASK)
XX nucleic acid molecules and encoded polypeptides. Cytostatic. The
XX antibody, oligopeptide or organic molecule that binds to the TASK
XX polypeptide are useful for treating a mammal having a tumour comprising
XX cells expressing the polypeptide. Antagonists of TASK are useful for
XX treating or preventing a cell proliferative disorder (e.g. cancer)
XX associated with increased expression or activity of TASK polypeptide. The
XX TASK polynucleotides and polypeptides may be used as hybridization probes
XX for isolating full length TASK DNA, for generating transgenic animals, in
XX chromosome identification, or for tissue typing. The present sequence
XX represents a human TASK polypeptide.

XX Sequence 543 AA;

Query Match 61.0%; Score 1655.5; DB 8; Length 543;

Best Local Similarity 59.9%; Pred. No. 1.6e-147;

Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;

QY 2 MSRDTKTSQ-----OSQGTSSSSSSAP-QSYSSSSSSTL 37

DB 1 MSRESDEAQQSHGSSACSPHGSVTSQSGSSSQSGISSSTSTMPNSSQSSHSSTL 60

QY 38 SSLDTPVQDLASI-----PEDPEIDEDIPQWGLMALGKFLNHDCLHEEYVGRDKK 92

DB 61 SSLETVSTQELYSIPEDQEPEDQEPPTAPWALMALQDGFANLECVNDNYWGRDKS 120

QY 93 CDYTFDIPVLNQTRYKTSKRHFRIFOELGHGHSRVANIEDLSGNGTFVFNKEIIGKRT 152

DB 121 CEYCFDEPLLKRTDKYRTSKKHFRIFREVGPKNSYIAYIEDHSGNGTFVNTLVGKGR 180

QY 153 LPLTNNAIALSLPNKVFVPSDLSDVDQTYPKDFIDKYIMSRPIGSGAGEVKLAFQK 212

DB 181 RPLNNSBIALSLSRNKVFVFDLTVDQSVYPKALRDEYIMSKTLGSGAGEVKLAFER 240

QY 213 SVCKKVAVKIISKRFKNTSSNEHP-ISVDTEIEILKLDHPCTIIKIENFDSDFYI 271

DB 241 KTCCKVAIKIISKRFKAIGSAREADPALNVETEIEILKLNHPCTIIKKNFDDAED-YII 299

QY 272 VLELMEGGELPDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPEENVLLSST 331

DB 300 VLELMEGGELPDKVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPEENVLLSQE 359

QY 332 BECCIKITDFGSKILGETSLMRTLCTGPTYLAPEVLNAGTGTGYSSAVDCWSLGVILFV 391

DB 360 EDCLIKITDFGHSKILGETSLMRTLCTGPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419

QY 392 CLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAFLVKNLLAVDPQRLTTKQ 451

DB 420 CLSGYPPFSEHRTQVSLKDOIITSGKNFPEWAEVSEKALDLVKKLVVDPKARFTTEE 479
 QY 452 ALBHPWLQDSMKHTVERLMYGVDMTHPPP---IKNNIIRKRGHEWDQDASTSS-----C 503
 DB 480 ALRHPWLQDEDMKRRKQDILLSEENESTALPQVLAQPSKSRKPREGEAGEAETTKRPVAVC 539
 QY 504 SEIL 507
 DB 540 AAVL 543
 RESULT 9
 ADO44010 standard; protein; 543 AA.
 AC ADO44010;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Amino acid sequence of human CHK2.
 XX
 KW protein complex; neurological disease; stroke; neurodegeneration;
 KW Wallerian degeneration; Alzheimer's disease; neurological disorder;
 KW epilepsy; inflammatory condition; ulcerative colitis; Crohn's disease;
 KW atherosclerosis; ID-MYO-inositol triphosphate 3 kinase A; ASK1; ASK2;
 KW ASK3; CaMKII beta; CaMKII delta; CaMKII gamma; casein kinase II alpha;
 KW Cdc37; CHK2; CTCL tumour antigen SE20-4; EF-1 alpha 1; EMAP;
 KW FLJ14653 NT2RP2002252; FLJ30839 FEBRA2002429; HERC2;
 KW inositol polyphosphate-5-phosphatase; inositol-1; 4;
 KW 5-triphosphate 5-phosphatase type 1; IRAK1; IRAK4; KIAA1441; MSTP030;
 KW Nek9; PAR3; Pellino 1; Pellino 3; podocalyxin-like protein 1 precursor;
 KW Pushover; S-adenosylhomocysteine;
 KW secretory carrier-associated membrane protein 2; surfactant protein 2;
 KW ubiquitin carboxyl terminal hydrolase 11;
 KW upstream regulatory element binding protein 1; Vartul;
 KW Werner's syndrome helicase interacting protein; WHIP;
 KW X-ray repair cross complementing protein 4.
 XX Homo sapiens.
 XX
 PN WO2004031242-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 11-SEP-2003; 2003WO-EP010110.
 XX
 PR 12-SEP-2002; 2002EP-00020495.
 PR 12-SEP-2002; 2002EP-00020496.
 PR 12-SEP-2002; 2002EP-00020497.
 XX
 PA (CELL-) CELLZOME AG.
 XX
 PI Boumeester T, Drewes G, Jackson D, Helftenbein G, Schirle M;
 PI Kuester B, Hopf C;
 XX
 DR WPI; 2004-316467/29.
 XX
 PT New complex comprising at least one first protein, and at least one
 PT second protein, useful for treating stroke, Alzheimer's disease,
 PT neurological disorders such as epilepsy, and inflammatory conditions such
 PT as ulcerative colitis.
 XX
 PS Example; Page 246-248; 287pp; English.
 XX
 CC The specification describes protein complexes involved in cellular
 CC processes which have been shown to be critical for the development of
 CC various forms of neurological diseases. Three protein complexes were
 CC identified: ASK2 protein complex, Pellino-1 protein complex and Pellino-3
 CC protein complex. The protein complex are useful for treating diseases and
 CC disorders, e.g. stroke, neurodegeneration such as Wallerian degeneration,
 CC Alzheimer's disease, neurological disorders such as epilepsy, and
 CC inflammatory conditions such as ulcerative colitis, Crohn's disease or

CC atherosclerosis. Proteins identified as being part of the protein
 CC complexes of the invention are ID-MYO-inositol triphosphate 3 kinase A,
 CC ASK1, ASK2, ASK3, CaMKII beta, CaMKII delta, CaMKII gamma, casein kinase
 CC II alpha, Cdc37, CHK2, CTCL tumour antigen SE20-4, EF-1 alpha 1, EMAP,
 CC FLJ14653 NT2RP2002252, FLJ30839 FEBRA2002429, HERC2, two hypothetical
 CC proteins of 35.5 kDa and 49.3 kDa, inositol polyphosphate-5-phosphatase,
 CC inositol-1,4,5-triphosphate 5-phosphatase type 1, IRAK1, IRAK4, KIAA1441,
 CC MSTP030, Nek9, PAR3, Pellino 1, Pellino 3, podocalyxin-like protein 1
 CC precursor, Pushover, a putative S-adenosylhomocysteine, secretory
 CC carrier-associated membrane protein 2, surfactant protein 2, ubiquitin
 CC carboxyl terminal hydrolase 11, upstream regulatory element binding
 CC protein 1, Vartul, Werner's syndrome helicase interacting protein (WHIP),
 CC X-ray repair cross complementing protein 4 (isoform 1). The present
 CC sequence represents CHK2.
 XX
 SQ Sequence 543 AA;
 Query Match 61.0%; Score 1655.5; DB 8; Length 543;
 Best Local Similarity 59.9%; Pred. No. 1.6e-147; Indels 39; Gaps 7;
 Matches 326; Conservative 74; Mismatches 105;
 QY 2 MSRDTKTESQ-----QSGTSSSSSSSSAP-QSYQSSSSGTL 37
 DB 1 MSRESDEVAQQSHGSSACSQPHGVTQSGSSSSQSGISSSTSTMPNSQSSSSGTL 60
 QY 38 SLSDTVVPQDLASI-----PEDEDEDIPQWRLWALGKGLNHDCLHEEYVVFORDKK 92
 DB 61 SSLETVSTQELYSIPEDQEPDEPEPTPAWRLWALQDGFANLECVDNWNVWFRDKS 120
 QY 93 CDYTPDIPVLCOTDRVKTYSKHFRIFOBLGHGHSRVANIEDLSNGTGTVNKEILCKGRT 152
 DB 121 CYCDEPLKRTDKRTYSKHFRIFEVGPNSYIAYIEDHSGNGTFTVTELVGKGR 180
 QY 153 LPLTNNAETALSLPNTKVFVFSDLSDVDDQTIYPKDPIDKYIMSRPIGSGACGEVKLAFOK 212
 DB 181 RLNNNSEIALSLRNKVFVFDLVDDQSVYPKALRDEYIMSKTSGSACGEVKLAER 240
 QY 213 SVCKKVAVKIIKRRKPKMNTSSNEHP-ISVDTEIEILKLDHPICIIKENFFDSEDFYI 271
 DB 241 KTKCKVAIKIISKRRKFAIGSAREADPALNVETEIEILKLNHPICIIKKNFFDAED-VYI 299
 QY 272 VLELMEGGELFDRVNVNSTLREPIAKLYFYOMLLAVOYLHENGVIHRDLKPENVLSSTS 331
 DB 300 VLELMEGGELFDKVNKRKLKATCKLYFYOMLLAVOYLHENGVIHRDLKPENVLSSOE 359
 QY 332 EECIKITDFGQSKILGETSLMRTLCGPTTYLAPEVLNTAGTTGYSSAVDCWSLGLVLFV 391
 DB 360 EDCLIKITDFGHSKILGETSLMRTLCGPTTYLAPEVLNVSGTAGYNRAVDCWSLGLVIF 419
 QY 392 CLCGYPPFSEHRTQVSLKDOIITSGKNFPEWAEVSEKALDLVKKLVVDPKARFTTEE 451
 DB 420 CLSGYPPFSEHRTQVSLKDOIITSGKNFPEWAEVSEKALDLVKKLVVDPKARFTTEE 479
 QY 452 ALBHPWLQDSMKHTVERLMYGVDMTHPPP---IKNNIIRKRGHEWDQDASTSS-----C 503
 DB 480 ALRHPWLQDEDMKRRKQDILLSEENESTALPQVLAQPSKSRKPREGEAGEAETTKRPVAVC 539
 QY 504 SEIL 507
 DB 540 AAVL 543
 RESULT 10
 ADOQ9232
 ID ADOQ9232 standard; protein; 543 AA.
 XX
 AC ADOQ9232;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human CHK2 protein SEQ ID NO:417.
 XX
 KW thanatos-associated protein; THAP; THAP responsive gene; THAP family;

THAP responsive element; angiogenesis; inflammation; metastasis; cancer; apoptosis; cardiovascular disease; neurodegenerative disease; chemokine; antiangiogenic; antiinflammatory; cardiovascular; cytostatic; neuroprotective; osteopathic; THAP modulator; THAP synthesis modulator; human.

Homo sapiens.
WO2004055050-A2.
01-JUL-2004.
10-DEC-2003; 2003WO-1B006434.
10-DEC-2002; 2002US-0432699P.
03-JUL-2003; 2003US-0485027P.
(ENDO-) ENDOCTUBE SAS.
(CNRS) CNRS CENT NAT RECH SCI.

Girard J, Amalric F, Roussigne M, Clouaire T;

WPI; 2004-525034/50.
N-PSDB; ADQ09233.

Modulating expression of a Thanatos (death)-Associated Protein (THAP) responsive gene for preventing or treating e.g. cancer or inflammation, comprises modulating the interaction of a THAP polypeptide with a nucleic acid.

Example 47; SEQ ID NO 417; 612pp; English.

The present invention describes a method for modulating the expression of a thanatos (death)-associated protein (THAP) responsive gene. The method comprises modulating the interaction of a THAP-family polypeptide or its biological fragment with a nucleic acid, and so enhancing or repressing the expression of the THAP responsive gene. Also described: (1) a method of modulating the expression of a gene responsive to a THAP/chemokine complex; (2) a pharmaceutical composition comprising a THAP responsive element in a pharmaceutical carrier; (3) a transcription factor decoy consisting essentially of a THAP responsive element; (4) a cell comprising a transcription factor decoy described above; (5) methods of modulating the interaction between a nucleic acid and a THAP-family polypeptide or its biological fragment, or a nucleic acid and a THAP/chemokine complex; (6) a vector packaging cell line comprising a cell comprising a viral vector which comprises a promoter operably linked to a nucleic acid encoding a THAP-family polypeptide or its biological fragment; (7) a method of constructing a cell which expresses a recombinant THAP-family polypeptide; (8) a method of ameliorating symptoms associated with a condition mediated by a THAP/chemokine complex; (9) methods of identifying a test compound that modulates transcription at a THAP responsive element or that modulates the transport of a chemokine into the nucleus; (10) methods for reducing the symptoms associated with a condition selected from excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive or insufficient apoptosis, cardiovascular disease and neurodegenerative diseases; symptoms associated with a condition resulting from the activity of a chemokine or a THAP-family polypeptide in an individual; or symptoms associated with transcriptional repression or activation mediated by a THAP-family polypeptide in an individual; (11) a vector comprising a THAP responsive promoter operably linked to a nucleic acid encoding a detectable product; (12) a genetically engineered cell comprising the vector described above or that expresses a THAP-family polypeptide or its biological fragment; (13) an in vitro transcription reaction comprising a nucleic acid comprising a THAP responsive promoter, ribonucleotides and an RNA polymerase; and (14) an isolated mutant THAP-family polypeptide that does not bind to a chemokine. The pharmaceutical composition has antiangiogenic, antiinflammatory, cardiovascular, cytostatic, neuroprotective and osteopathic activities, and can be used as a THAP and THAP synthesis modulator. The composition can be used for modulating the expression of a THAP responsive gene. Modulation is useful for reducing symptoms of conditions such as excessive or insufficient angiogenesis, inflammation, metastasis of a cancerous tissue, excessive

CC or insufficient apoptosis, cardiovascular disease or neurodegenerative diseases. The present sequence is used in the exemplification of the present invention.
XX Sequence 543 AA;

Query Match
Best Local Similarity 61.0%; Score 1655.5; DB 8; Length 543;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTESQ-----SQGTSSSSSSSAP-QSYSSSSSSTL 37
Db 1 MSRESDEAQQSHGSSACSQPHGSVTSQSSSSQSGISSSTSTMPNSSQSSSSSTL 60
QY 38 SSLDTVPVODLASI-----PEDPEIDEDIPOPWGLWALGKGLNHDCLHEEYVFGDKK 92
Db 61 SSLETVSTQELYSIPEDQEPPEPTAPWARKWALQDGFANLETCVNONYVFGDKS 120
QY 93 CDYTFDIPVLNQTORYKTYSKRHFRIFOELGHGHSRVANIEDLSGNGTFVFNKEIIGKGT 152
Db 121 CEYCFDEPLLKRTDKYRTYSKKHFRIFREVGPKNSYIAIEDHSGNGTFVATELVGKGR 180
QY 153 LPLTNNAEIALSLPTNKVVFSDLSVDQTYTPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
Db 181 RPLNNSBIALSLSRNKVVFDFLTVDQSVYPKALRDEYIMSKTLGSGACGEVKLAF 240
QY 213 SVCKKAVAKIISKRFKNTSSNEHP-ISTVTEIEILKLDHPCLIKIENPFDSDFYI 271
Db 241 KTCCKVAIKIISKRFKNTSSNEHP-ISTVTEIEILKLDHPCLIKIENPFDSDFYI 299
QY 272 VLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPNVLLSSTS 331
Db 300 VLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRDLKPNVLLSSTS 359
QY 332 BECCIKITDFGSKILGTSLMRTLCGPTTYLAPBLVNTAGTTGVSADVCSLGVILFV 391
Db 360 EDCLIKITDFGSKILGTSLMRTLCGPTTYLAPBLVNTAGTTGVSADVCSLGVILFV 419
QY 392 CLCGVPPFSEQNSNIPKNOIAEGKYTYIAAARNVSEQAPDLVKNLAVDPPEQLTTKO 451
Db 420 CLSGPPFSEHRTQVSLKDKITSGKINFPEWAEVSEKALDLVKLLVDPKARFTTE 479
QY 452 ALEHPWLQDDSMKHTVERLMYGVDMTPPP---TKNIIIRKRGHEWDDQASTSS----C 503
Db 480 ALRHEPWLQDDSMKHTVERLMYGVDMTPPP---TKNIIIRKRGHEWDDQASTSS----C 503
QY 504 SEIL 507
Db 540 AAVL 543

RESULT 11
AA48996
ID AA48996 standard; protein; 543 AA.
XX
AC AA48996;
XX
DT 08-JUL-2002 (first entry)
XX
DE Human Chk2 phosphoenzyme inhibitor related protein #2.
XX
KW Human; Chk2 phosphoenzyme inhibitor; cytostatic.
XX
OS Homo sapiens.
XX
PN JP2001346588-A.
XX
PD 18-DEC-2001.
XX
PF 08-JUN-2000; 2000JP-00172273.
XX
PR 08-JUN-2000; 2000JP-00172273.
XX

PA	(IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.	
XX	WPI; 2002-145186/19.	
DR	N-PSDB; AAL44751.	
XX		
XX	New gene encoding a protein for inhibiting human Chk2 phosphoenzyme activity.	
PT		
XX		
PS	Disclosure; Page 27-30; 36pp; Japanese.	
XX		
CC	The present invention provides the protein and coding sequences of a human Chk2 phosphoenzyme inhibitor. The sequences can be used in the chemotherapy of cancers. The present sequence is a protein described in the exemplification of the invention	
XX		
SQ	Sequence 543 AA;	
	Query Match 60.9%; Score 1651.5; DB 5; Length 543;	
	Best Local Similarity 59.7%; Pred. No. 3.8e-147;	
	Matches 325; Conservative 75; Mismatches 105; Indels 39; Gaps 7;	
QY	2 MSRDTKTESQ-----QSQGTSSSSSSAP-QSYQSSSSGTL 37	
Db	1 MSRESDEAQQSHGSSACSQPHGSVTQSGSSSQSGISSTSTMPNSQSSHSSGTL 60	
QY	38 SSLDTVPVQDLASI-----PEDPEIDEDIPQWGRWLWALGKFLNHDCLHEEYVFGDKK 92	
Db	61 SLSLETSTQELYSIPEDQEPDEPPTAPWALWALQDGFANLECVNDNYWFGDKS 120	
QY	93 CDYTFDIPVLNODRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVKNELICKGRT 152	
Db	121 CEYCFDEPLDKRTDYKTYSKRHFRIFREVGPKNSYIAYIEDHSGNGTFVTELVGKGR 180	
QY	153 LPLTNNAEIALSLPTNKVFVFSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQ 212	
Db	181 RPLNNSEIALSLRNKVFVFFDLTVDDQSVYPKALRDEYIMSKTIGSGACGEVKLAF 240	
QY	213 SVCKKVAVKIISKRFKPMNTSSNEHP- ISVDTEILKLDHPICIIKIENFDSDFYI 271	
Db	241 KTCKKVAIKIISKRFKFAIGSAREADPALNVETEILKLNHPICIIKKNFFDAED-YYI 299	
QY	272 VLELMGGELFDRVNVNSTRLREPFAKLYFQYOMLLAVOYLHENGVIHRDLKPENVLSS 331	
Db	300 VLELMGGELFDRVNVNSTRLREPFAKLYFQYOMLLAVOYLHENGVIHRDLKPENVLSS 359	
QY	332 EECIKITDFQGSKILGETSLMRTLCGTPPYLAPELVNLTAGTGYSSAVDCMSLGVILFV 391	
Db	360 EDCLIKITDFGHSKILGETSLMRTLCGTPPYLAPELVNLTAGTGYSSAVDCMSLGVILF 419	
QY	392 CLCGYPPFPSSQNSNIPKIQIAGKYTYIAAARNVSEQAFDLVKNLLVVDPEQLRTTKQ 451	
Db	420 CLSGYPPFPSSHRTQVSLKDQITSGKYNFIPVWAEVSEKALDLVKLLVVDPKARFTTE 479	
QY	452 ALRHPWLQDDSMKHTVERLMYGVNHTMPP- --IKNNIRKRGHEWDDQASTSS- ---C 503	
Db	480 ALRHPWLQDDMKRKFQDILLSEENESTALPQVLAQPSRKRPRGEAGEAETTKRPV 539	
QY	504 SEIL 507	
Db	540 AAVL 543	
	RESULT 12	
ID	AAV67968	
XX	AAV67968 standard; protein; 543 AA.	
AC	AAV67968;	
XX		
DT	05-APR-2000 (first entry)	
XX		
DE	Human cell cycle regulatory factor Cds1 SEQ ID NO:1.	
XX		
KW	Human; cell cycle regulatory factor; Cds1; hcds1; cdc25; histone H1;	
	phosphorylation; cancer; proliferative disease; cytostatic; gene therapy.	
KW	Homo sapiens.	
OS	WO9967369-A1.	
PN	29-DEC-1999.	
PD		
XX		
PF	23-JUN-1999; 99WO-JP003350.	
XX		
PR	23-JUN-1999; 98JP-00192467.	
XX		
PA	(CHUS) CHUGAI SEIYAKU KK.	
PI	Nakanishi M;	
XX		
DR	WPI; 2000-106292/09.	
DR	N-PSDB; AA257411.	
XX		
PT	Cell cycle regulatory factor-encoding gene for production recombinant proteins with kinase activity, used to develop drugs to treat cancers and proliferative diseases.	
PT		
XX		
PS	Claim 1; Page 35-39; 52pp; Japanese.	
XX		
CC	The present sequence represents the human cell cycle regulatory factor Cds1. The Cds1 nucleotide sequence can be used in gene therapy. Cds1 may be used to detect inhibitors of cell cycle regulatory factors which can be applied in the development of drugs for treating cancers and proliferative diseases. Cds1 is strongly expressed in the testis as well as other tissues. Cds1 can efficiently phosphorylate cdc25 and histone H1	
XX		
SQ	Sequence 543 AA;	
	Query Match 60.6%; Score 1643.5; DB 3; Length 543;	
	Best Local Similarity 59.6%; Pred. No. 2.2e-146;	
	Matches 325; Conservative 75; Mismatches 104; Indels 41; Gaps 8;	
QY	2 MSRDTKTESQ-----QSQGTSSSSSSAPQSYQSS--SSGT 36	
Db	1 MSRESDEAQQSHGSSACSQPHGSVTQSGSSSQSGISSTSTMPNS-QSSHPSSGT 59	
QY	37 LSSLTVPVQDLASI-----PEDPEIDEDIPQWGRWLWALGKFLNHDCLHEEYVFGDK 91	
Db	60 LSSLETSTQELYSIPEDQEPDEPPTAPWALWALQDGFANLECVNDNYWFGDK 119	
QY	92 KCDYTFDIPVLNODRYKTYSKRHFRIFQELGHGHSRVANIEDLSGNGTFVKNELICKGR 151	
Db	120 SCEYCFDEPLDKRTDYKTYSKRHFRIFREVGPKNSYIAYIEDHSGNGTFVTELVGKGR 179	
QY	152 TLPLTNNAEIALSLPTNKVFVFSVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQ 211	
Db	180 RPLNNSEIALSLRNKVFVFFDLTVDDQSVYPKALRDEYIMSKTIGSGACGEVKLAF 239	
QY	212 KSVCKKVAVKIISKRFKPMNTSSNEHP- ISVDTEILKLDHPICIIKIENFDSDFY 270	
Db	240 RTCKKVAIKIISKRFKFAIGSAREADPALNVETEILKLNHPICIIKKNFFDAED-YY 298	
QY	271 IVLELMGGELFDRVNVNSTRLREPFAKLYFQYOMLLAVOYLHENGVIHRDLKPENVLSS 330	
Db	299 IVLELMGGELFDRVNVNSTRLREPFAKLYFQYOMLLAVOYLHENGVIHRDLKPENVLSS 358	
QY	331 SBECCIKITDFQGSKILGETSLMRTLCGTPPYLAPELVNLTAGTGYSSAVDCMSLGVILF 390	
Db	359 EEDCLIKITDFGHSKILGETSLMRTLCGTPPYLAPELVNLTAGTGYSSAVDCMSLGVILF 418	
QY	391 VCLCGYPPFPSSQNSNIPKIQIAGKYTYIAAARNVSEQAFDLVKNLLVVDPEQLRTTK 450	
Db	419 ICLSGYPPFPSEHRTQVSLKDQITSGKYNFIPVWAEVSEKALDLVKLLVVDPKARFTTE 478	
QY	451 QALEHPWLQDDSMKHTVERLMYGVNHTMPP- --IKNNIRKRGHEWDDQASTSS- --- 502	
Db	479 EALRHPWLQDDMKRKFQDILLSEENESTALPQVLAQPSRKRPRGEAGEAETTKRPV 538	

QY 503 CSEIL 507
Db 539 CAAVL 543

RESULT 13
ADN61455
ID ADN61455 standard; protein; 586 AA.
AC ADN61455;
XX
DT 12-AUG-2004 (first entry)
DE Human KPP-21 protein SEQ ID NO:21.
KW human; kinase; phosphatase; enzyme; KPP; cytostatic;
KW antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;
KW cerebroprotective; anti-HIV; anti-allergic; antiinflammatory;
KW thymimetic; gene therapy; cell proliferative disorder; cancer;
KW atherosclerosis; neurological disorder; epilepsy; Huntington's disease;
KW stroke; immune disorder; inflammatory disorder; AIDS; allergy;
KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection.
OS Homo sapiens.
XX
PN WO2004040222-A2.
XX
PD 21-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034809.
XX
PR 01-NOV-2002; 2002US-0423226P.
PR 15-NOV-2002; 2002US-0426713P.
PR 26-NOV-2002; 2002US-0429766P.
PR 11-FEB-2003; 2003US-0447043P.
XX
(INCY-) INCYTE CORP.
XX
PI Hafalia AJA, Lee S, Murage J, Swarnakar A, Chawla NK, Khare R;
PI Elliott VS, Tran UK, Ramkumar J, Gururajan R, Baughn MR, Gletzen KJ;
PI Yang YG, Chien D, Wang JT, Favero KD, Becha SD, Richardson TW;
PI Jin P, Hawkins PR, Yue H, Lee EA, Marquis JP;
XX
DR WPI; 2004-390608/36.
DR N-PSDB; ADN61511.
XX
PT New human kinases and phosphatases (KPP), useful for diagnosing, treating
PT and preventing diseases or conditions associated with the aberrant KPP
PT expression e.g. cancer, AIDS, epilepsy, or infections.
XX
PS Claim 1; SEQ ID NO 21; 320pp; English.
XX
CC The present sequence represents a human kinase and phosphatase protein
CC designated KPP-21. Human KPP sequences have cytostatic,
CC antiarteriosclerotic, anticonvulsant, nootropic, neuroprotective,
CC cerebroprotective, anti-HIV, anti-allergic, antiinflammatory and
CC thymimetic activities, and can be used in gene therapy. The human KPP
CC polypeptides and polynucleotides of the invention are useful in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of KPP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)
CC disorders, or infections. They are also useful in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of KPP. The KPP sequences or their fragments are useful in
CC screening compounds for effectiveness as agonist or antagonist of the
CC polypeptides, or in altering the expression of the target polynucleotide
CC and compounds that specifically bind to or modulate the activity of the
XX polypeptide.
XX
SQ Sequence 586 AA;

Query Match 59.9%; Score 1624; DB 8; Length 586;
Best Local Similarity 55.5%; Pred. No. 1.7e-144;
Matches 326; Conservative 74; Mismatches 105; Indels 82; Gaps 8;

QY 2 MSRTKTESQ-----SQGTSSSSSSSAP-QSYSSSSSSTL 37
Db 1 MSRESDEAQQSHGSSACSPHGSVTSQSSSSQSGTSSSTMPNSSQSSSSSSTL 60
QY 38 SSLLDTVPVQDLASI-----PEDPEIDEDIPOPWRLWALGKFLNHD----- 79
Db 61 SSLETVTSTQELYSIPEDQEPPEEPTPAPWRLWALQDGFANLETESGHVTSQDLLEL 120
QY 80 -----CLHEEYVFEGRDKKCDYTFDIPVLNQTDYK 109
Db 121 LLSDDPPASASQAGIRGVRHHPVCSLKCVDNMYWGRDKSEYCFDEPLKRTDKYR 180
QY 110 TYSKRHPRIPOELGHGHSRVANIIDLSONGTFTVKEIIGKRTPLTNNAEIALSLPTNK 169
Db 181 TYSKKHFRIPREVGPKNSYIAYIEDHSGNGTFTVNTLVGKRRRPLNNSSEIALSLSRNK 240
QY 170 VFVFSDLSDVDDOTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKKAVKIISKRFK 229
Db 241 VFVFFDLTVDDQSVYPKALRDEYIMSKTGLSGACGEVKLAFERTCKKVAKIISKRKPA 300
QY 230 MNTSSNEHP-ISVDTEIEILKKLDHPCCI KIENFFDSDFYIIVLELMEGGELFDRVYNS 288
Db 301 IGSAREADPALNVETEIEILKKLNHPCCI KIKNFFDAED-YIIVLELMEGGELFDRVYNS 359
QY 289 TRLREPTAKLYFYQMLLAVALYHENGVIHRLKPEVLLSSTSECCIKITDFGOSKILG 348
Db 360 KRLKEATCKLYFYQMLLAVALYHENGVIHRLKPEVLLSSTSECCIKITDFGOSKILG 419
QY 349 ETSLMRTLCGTPTYLAPVLNTAGTGYSSAVDCWSLGVILFVCLCGYPPPESEQNSIPL 408
Db 420 ETSLMRTLCTGPTYLAPVLVSVGTAGYNRAVDCWSLGVILFVCLSGYPPPESEHRTQSL 479
QY 409 KNQIAEGKYTYIAAAWRNVSEQAFDLVKNLLVDPPEQRLLTKQALEHPWLQDSDMKHTVE 468
Db 480 KDQITSGKYNFIPEWAEVSEKALDLVKLLVDPKARFTTEALRHPWLQDSDMKRKFQ 539
QY 469 RLMTGVDMTHPPP---IKNNIRKRGHEWDOQASTSS-----CSEIL 507
Db 540 DLLSEENESTALPQVLAQPSTSRKRPRGEAGEAETTKRPAVCAAVL 586

RESULT 14
AAM48994
ID AAM48994 standard; protein; 514 AA.
XX
AC AAM48994;
XX
DT 08-JUL-2002 (first entry)
XX
DE Human Chk2 phosphoenzyme inhibitor.
XX
KW Human; Chk2 phosphoenzyme inhibitor; cytostatic.
XX
OS Homo sapiens.
XX
PN JP2001346588-A.
XX
PD 18-DEC-2001.
XX
PF 08-JUN-2000; 2000JP-00172273.
XX
PR 08-JUN-2000; 2000JP-00172273.
XX
PA (IGAK-) IGAKU SEIBUTSUGAKU KENKYUSHO KK.
XX
DR WPI; 2002-145186/19.
DR N-PSDB; AAL44749.
XX

QY 121 ELGHHGHSRVANTIEDLSGNGTFFVNKEIIGKGRTPLTNNAEIALSLPTNKKVFVFSLSVDD 180
DB 121 ELGHHGHSRVANTIEDLSGNGTFFVNKEIIGKGRTPLTNNAEIALSLPTNKKVFVFSLSVDD 180
QY 181 QTIYPKDFTDKYMRSRPIGSGACGEVKLAFQSVCKKVAVKIISKRKFQNTSSNEHPIS 240
DB 181 QTIYPKDFTDKYMRSRPIGSGACGEVKLAFQSVCKKVAVKIISKRKFQNTSSNEHPIS 240
QY 241 VTEIEILKLDHPICIIKENFDFSEDFFYIIVLELMEGGELFDRVNVNSTRLEPITAKLYF 300
DB 241 VTEIEILKLDHPICIIKENFDFSEDFFYIIVLELMEGGELFDRVNVNSTRLEPITAKLYF 300
QY 301 YQMLLAVOYLHENGVIHRDLKPEENVLLSSTSECCIKITDFQSKILGETSLMRTLCTGP 360
DB 301 YQMLLAVOYLHENGVIHRDLKPEENVLLSSTSECCIKITDFQSKILGETSLMRTLCTGP 360
QY 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFPSEQNSNIPLNQIAEGKYTYI 420
DB 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFPSEQNSNIPLNQIAEGKYTYI 420
QY 421 AAARNVSEQAFDLVKNLLVDPPEORLTTKQALEHPWLQDDSMKHTVERLMYGVVHTMPP 480
DB 421 AAARNVSEQAFDLVKNLLVDPPEORLTTKQALEHPWLQDDSMKHTVERLMYGVVHTMPP 480
QY 481 PIKNIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517
DB 481 PIKNIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517

RESULT 2

US-10-618-173-2
; Sequence 2, Application US/10618173
; Publication No. US20040018603A1
; GENERAL INFORMATION:
; APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
; APPLICANT: GUO, Zijian
; APPLICANT: DUNPHY, William
; TITLE OF INVENTION: CHECKPOINT-ACTIVATING OLIGONUCLEOTIDES
; FILE REFERENCE: CITI350-1
; CURRENT APPLICATION NUMBER: US/10/618,173
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: US/09/849,617
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: US 60/202,028
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-10-618-173-2

Query Match 100.0%; Score 2712; DB 15; Length 517;
Best Local Similarity 100.0%; Pred. No. 3.5e-193;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MMSRDTKTESQSQGTSSTSSSSAPQSYQSSSGTSLSDTPVPQDLASIPEDPEIDED 60
DB 1 MMSRDTKTESQSQGTSSTSSSSAPQSYQSSSGTSLSDTPVPQDLASIPEDPEIDED 60
QY 61 IPQWGRWLWALGKFLNHDCLHEEYVFGDKKCDYTFDIPVLNQTDTRYKTSKRHFRIQ 120
DB 61 IPQWGRWLWALGKFLNHDCLHEEYVFGDKKCDYTFDIPVLNQTDTRYKTSKRHFRIQ 120
QY 121 ELGHHGHSRVANTIEDLSGNGTFFVNKEIIGKGRTPLTNNAEIALSLPTNKKVFVFSLSVDD 180
DB 121 ELGHHGHSRVANTIEDLSGNGTFFVNKEIIGKGRTPLTNNAEIALSLPTNKKVFVFSLSVDD 180
QY 181 QTIYPKDFTDKYMRSRPIGSGACGEVKLAFQSVCKKVAVKIISKRKFQNTSSNEHPIS 240
DB 181 QTIYPKDFTDKYMRSRPIGSGACGEVKLAFQSVCKKVAVKIISKRKFQNTSSNEHPIS 240

QY 241 VTEIEILKLDHPICIIKENFDFSEDFFYIIVLELMEGGELFDRVNVNSTRLEPITAKLYF 300
DB 241 VTEIEILKLDHPICIIKENFDFSEDFFYIIVLELMEGGELFDRVNVNSTRLEPITAKLYF 300
QY 301 YQMLLAVOYLHENGVIHRDLKPEENVLLSSTSECCIKITDFQSKILGETSLMRTLCTGP 360
DB 301 YQMLLAVOYLHENGVIHRDLKPEENVLLSSTSECCIKITDFQSKILGETSLMRTLCTGP 360
QY 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFPSEQNSNIPLNQIAEGKYTYI 420
DB 361 TYLAPEVLNTAGTTGYSSAVDCWSLGVILFVCLCGYPPFPSEQNSNIPLNQIAEGKYTYI 420
QY 421 AAARNVSEQAFDLVKNLLVDPPEORLTTKQALEHPWLQDDSMKHTVERLMYGVVHTMPP 480
DB 421 AAARNVSEQAFDLVKNLLVDPPEORLTTKQALEHPWLQDDSMKHTVERLMYGVVHTMPP 480
QY 481 PIKNIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517
DB 481 PIKNIIRKRGHEWDQDASTSSCSSEILPTSAEKRAKR 517

RESULT 3

US-10-185-182A-2
; Sequence 2, Application US/10185182A
; Publication No. US20030017160A1
; GENERAL INFORMATION:
; APPLICANT: LUYTEN, Walter H.M.L.
; APPLICANT: PARKER, Andrew E.
; APPLICANT: MCGOWAN, Clare H.
; APPLICANT: BLASINA, Alessandra
; TITLE OF INVENTION: HUMAN CHECKPOINT KINASE, hCDS1,
; FILE REFERENCE: TSRI 649.0 Div.1
; CURRENT APPLICATION NUMBER: US/10/185,182A
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: US 09/529,093
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/EP98/06981
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: GB 9722320.0
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-185-182A-2

Query Match 61.0%; Score 1655.5; DB 14; Length 543;
Best Local Similarity 59.9%; Pred. No. 1.5e-114;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;

QY 2 MSRDTKTESQ-----QSQGTSSTSSSSAP-QSYQSSSGTSL 37
DB 1 MSRESDEVAQSHGSSACSQPHGVSVTQSGSSSQSGISSSTSTMPNSSQSSSGT 60
QY 38 SSLDTPVPQDLASI-----PEDPEIDEDIPQWGRWLWALGKFLNHDCLHEEYVFGDKK 92
DB 61 SSLETVTQELYSIPEDQPEEPETTPAWRLMALQDGFANLECVDNDYVTFGRDKS 120
QY 93 CDYTPDIPVLNQTDTRYKTSKRHFRIQELGHHGHSRVANIEDLSGNGTFFVNKEIIGKRT 152
DB 121 CEYCFDEPLLKXETDKYRIYSKKGFRIREVGPKNYSIAVIEDHSGNGTFFVNTLVGKGR 180
QY 153 IPLTNNAEIALSLPTNKKVFVFSLSVDDQTYPKDFIDKYMRSRPIGSGACGEVKLAFQ 212
DB 181 RPLNNNSIALSLSNKVFVFFDLTVDDQSVYPKALRDEYIMSKTIGSGACGEVKLAF 240
QY 213 SVCKKVAVKIISKRKFQNTSSNEHP-ISVDTEIEILKLDHPICIIKENPFDSEDFYI 271
DB 241 KTCCKVAVKIISKRKFQNTSSNEHP-ISVDTEIEILKLDHPICIIKENPFDSEDFYI 299

QY 272 VLEMEGGELFDRVNSTRLREPIAKLYFYQMLLA VOYLHENGVIHRDLKPENVLSSSTS 331
Db 300 VLEMEGGELFDRVNGKRLKEATCKLYFYQMLLA VOYLHENGVIHRDLKPENVLSSQE 359
QY 332 EECCKITDFGOSKILGETSLMRTLCGTPTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 391
Db 360 EDCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419
QY 392 CLCGYPPFSEQNSNIPLNQIABGKTYTAAAWRNVSEQAFDLVKNLLVVDPEQRITTKQ 451
Db 420 CLSGYPPFSEHRTQVSLKDQITSGKYNFIPEVMAEVSEKALDLVKLLVVDPKARPTTEE 479
QY 452 ALRHPWLQDDSMKHTVERLMYGVHDHTMPP---IKKNIIRKKGHEWDQDASTSS---C 503
Db 480 ALRHPWLQDDMKRFQDLLSEENESTALPQVLAQPSRKPRGEAGEAETTKRPVAVC 539
QY 504 SEIL 507
Db 540 AAVL 543

RESULT 4

US-10-733-878-417
; Sequence 417, Application US/10733878
; Publication No. US20040224408A1
; GENERAL INFORMATION:
; APPLICANT: Jean-Philippe Girard
; APPLICANT: Francois Amalric
; APPLICANT: Myriam Roussigne
; APPLICANT: Thomas Clouaire
; TITLE OF INVENTION: THAP PROTEINS AS NUCLEAR RECEPTORS FOR
; TITLE OF INVENTION: CHEMOKINES AND ROLES IN TRANSCRIPTIONAL REGULATION, CELL
; FILE OF INVENTION: PROLIFERATION AND CELL DIFFERENTIATION
; FILE REFERENCE: BIOBANK-012A
; CURRENT APPLICATION NUMBER: US/10/733,878
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 60/432699
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: 60/485027
; PRIOR FILING DATE: 2003-07-03
; NUMBER OF SEQ ID NOS: 535
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 417
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-733-878-417

Query Match 61.0%; Score 1655.5; DB 16; Length 543;
Best Local Similarity 59.9%; Pred. No. 1.5e-114;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTESQ-----QSGTSSSSSSSAP-OSYSSSSSGTL 37
Db 1 MSRESDEVAQSHGSSACSQPHGSVTQSGSSSQSGISSSSTSTMPNSSQSHSSGTL 60
QY 38 SSLDTVPVQDLASI-----PEDPEIDEDIPQWGRWLWALGKGLNHDCLHEEYVFGDRKK 92
Db 61 SLETVSTQELYSIPEDQEPEDQPEPTPAPARLWALQDGFANLECVNDNWFGRDKS 120
QY 93 CDYTFDIPVLNQTRKYTSKHFRIQELGCHGSHRVANIEDLSGNGTFVNKEIIKGRT 152
Db 121 CEYCFDEPLKRTDKYRTYSKHFRIPEVGPKNYSIAYIEDSHGNGTFVNTLVGKGR 180
QY 153 LPLTNNAEIALSLPTNKVFVSDLSVDDDTIYPKDFIDKYIMSRPIGSGACGEVKLAFQ 212
Db 181 RPLNNSEIALSLSRNKVFFVFDLTVDQSVYPKALRDEYIMSKTLGSGACGEVKLAF 240
QY 213 SVCKYVAVKIIISKRKFQWNTSSNEHP-ISVDTEIELKLDHPICIIKENFDSDFYI 271
Db 241 KTCKYVAVKIIISKRKAIGSAREADPALNVETEIELKLNHFCIIKKNFFDAED-YVI 299
QY 272 VLEMEGGELFDRVNSTRLREPIAKLYFYQMLLA VOYLHENGVIHRDLKPENVLSSSTS 331

Db 300 VLEMEGGELFDRVNGKRLKEATCKLYFYQMLLA VOYLHENGVIHRDLKPENVLSSQE 359
QY 332 EECCKITDFGOSKILGETSLMRTLCGTPTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 391
Db 360 EDCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419
QY 392 CLCGYPPFSEQNSNIPLNQIABGKTYTAAAWRNVSEQAFDLVKNLLVVDPEQRITTKQ 451
Db 420 CLSGYPPFSEHRTQVSLKDQITSGKYNFIPEVMAEVSEKALDLVKLLVVDPKARPTTEE 479
QY 452 ALRHPWLQDDSMKHTVERLMYGVHDHTMPP---IKKNIIRKKGHEWDQDASTSS---C 503
Db 480 ALRHPWLQDDMKRFQDLLSEENESTALPQVLAQPSRKPRGEAGEAETTKRPVAVC 539
QY 504 SEIL 507
Db 540 AAVL 543

RESULT 5

US-10-820-583A-2
; Sequence 2, Application US/10820583A
; Publication No. US20040242461A1
; GENERAL INFORMATION:
; APPLICANT: Schneider, Michael
; APPLICANT: Oh, Hidemasa
; TITLE OF INVENTION: Modulators of Telomere Stability
; FILE REFERENCE: HO-P02673US1
; CURRENT APPLICATION NUMBER: US/10/820,583A
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/461,095
; PRIOR FILING DATE: 2003-04-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Human
US-10-820-583A-2

Query Match 61.0%; Score 1655.5; DB 16; Length 543;
Best Local Similarity 59.9%; Pred. No. 1.5e-114;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTESQ-----QSGTSSSSSSSAP-OSYSSSSSGTL 37
Db 1 MSRESDEVAQSHGSSACSQPHGSVTQSGSSSQSGISSSSTSTMPNSSQSHSSGTL 60
QY 38 SSLDTVPVQDLASI-----PEDPEIDEDIPQWGRWLWALGKGLNHDCLHEEYVFGDRKK 92
Db 61 SLETVSTQELYSIPEDQEPEDQPEPTPAPARLWALQDGFANLECVNDNWFGRDKS 120
QY 93 CDYTFDIPVLNQTRKYTSKHFRIQELGCHGSHRVANIEDLSGNGTFVNKEIIKGRT 152
Db 121 CEYCFDEPLKRTDKYRTYSKHFRIPEVGPKNYSIAYIEDSHGNGTFVNTLVGKGR 180
QY 153 LPLTNNAEIALSLPTNKVFVSDLSVDDDTIYPKDFIDKYIMSRPIGSGACGEVKLAFQ 212
Db 181 RPLNNSEIALSLSRNKVFFVFDLTVDQSVYPKALRDEYIMSKTLGSGACGEVKLAF 240
QY 213 SVCKYVAVKIIISKRKFQWNTSSNEHP-ISVDTEIELKLDHPICIIKENFDSDFYI 271
Db 241 KTCKYVAVKIIISKRKAIGSAREADPALNVETEIELKLNHFCIIKKNFFDAED-YVI 299
QY 272 VLEMEGGELFDRVNSTRLREPIAKLYFYQMLLA VOYLHENGVIHRDLKPENVLSSSTS 331
Db 300 VLEMEGGELFDRVNGKRLKEATCKLYFYQMLLA VOYLHENGVIHRDLKPENVLSSQE 359
QY 332 EECCKITDFGOSKILGETSLMRTLCGTPTYLAPEVLNTAGTGYSSAVDCWSLGVILFV 391
Db 360 EDCLIKITDFGHSKILGETSLMRTLCGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFI 419

QY 392 CLCGYPPFSEBQNSIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKLLVDPPEQLRTTKQ 451
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
420 CLSGYPPFSEHRTQVSLKDQITSGKYNFIPEVWAEVSEKALDLVKLLVDPDKARFTTEE 479
QY 452 ALEHFWLQDDSMKHTVERLMYGVDMHTMPP-----IKNIIRKRGHEWDQDASTSS-----C 503
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
480 ALRHPWLQDEDMKRFQDILLSENESTALPQVLAQFSTSRKRPRGEAGAEFTTKRPAVC 539
QY 504 SEIL 507
Db : : : : :
540 AAVL 543
RESULT 6
US-10-142-356-6
; Sequence 6, Application US/10142356
; Publication No. US20030036183A1
; GENERAL INFORMATION:
; APPLICANT: Boylan, John F.
; TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40
; FILE REFERENCE: 01017/37177A
; CURRENT APPLICATION NUMBER: US/10/142,356
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 60/290,276
; PRIOR FILING DATE: 2001-05-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 545
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-142-356-6

Query Match 60.6%; Score 1644.5; DB 14; Length 545;
Best Local Similarity 63.0%; Pred. No. 9.8e-114;
Matches 327; Conservative 69; Mismatches 108; Indels 15; Gaps 7;
QY 3 SDDTKTESQ-----SQSGTSSSSSSSAP-QSYSSSSSSGTLSSLTVPQDLASIPEDPE 56
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
28 SOSQGTSPQLHLSQVQGHASSSTSTVPSSSSSHSSGTLSSLTSTVQELCSIPEDQE 87
QY 57 IDEDIPQPMGRWLWALGKGLHNDCLHEEYVFGDKDYTFDIPVLNQDRTYKTKSRHF 116
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
88 PEEPTGPWRLWALQDGSNLDVNDNWFGRDKSCEYCPDGLLKRDKRTYVSKGHF 147
QY 117 RFQELGHGHSRVANIEDLSNGTGFVNKEIGKRTLPLTNNAEIALSLPTNKKVVFSDL 176
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
148 RIFREMGPKNCYIVYLEDSHSGNGTFVNTLIGKGRCLPLNNSEIALSLCRNKVVFDDL 207
QY 177 SVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQKSVCKVAVKIISSKRKFMMNTSSN- 235
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
208 TVDDQSVYKPEURDEYIMSKTIGSGACGEVKAFERKTKKVAIKIISRRFALGSSREA 267
QY 236 EHPISVDTIEILKLDHPDIIKIENFFDSEFYIIVLEMEGGELDFRVVNSTRLEPI 295
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
268 DTAPSVETEIEILKXLNHFCIIKIKDVFDED-YIIVLEMEGGELFORVVGKRLKEAT 326
QY 296 AKLYFYQMLLAQVYLHENGVIHRDLKPENVLSSSTSEBCCIKITDQSGKILGETSLMRT 355
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
327 CKLYFYQMLLAQVYLHENGIIHRDLKPENVLSSQEECLIKITDQSGKILGETSLMRT 386
QY 356 LCGTPTYLAPENLTAGTGYSSAVDCWSLGVTLFVCLGYPPEFSEQNSIPLKNQIAEG 415
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
387 LCGTPTYLAPENLISNGTAGYGRVDCWSLGVTLFCLSGYPPFSEHKTQVSLKQDITSG 446
QY 416 KYTYIAAAWRNVSEQAFDLVKLLVDPPEQLRTTKQALEHFWLQDDSMKHTVERLMYGVDM 475
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
447 KYNLPEVWTVDSSEKALDLVKLLVDPDKARFTTEEALSHPWLDHEMKKFKQDLVQEK 506
QY 476 HTWPPPI--KNIIRKRGHEWD-QDASTSS-----CSEIL 507
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
507 NLVPLPAPQTSQGRPLELEAEDAESSKRLAVCKAVL 545

RESULT 7
US-09-740-627-1
; Sequence 1, Application US/09740627
; Patent No. US20020012964A1
; GENERAL INFORMATION:
; APPLICANT: Nakanishi, Makoto
; TITLE OF INVENTION: CELL CYCLE REGULATING FACTOR
; FILE REFERENCE: 06501-071001
; CURRENT APPLICATION NUMBER: US/09/740,627
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: PCT/JP99/03350
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: JP 10/192467
; PRIOR FILING DATE: 1998-06-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-627-1
Query Match 60.6%; Score 1643.5; DB 9; Length 543;
Best Local Similarity 59.6%; Pred. No. 1.2e-113;
Matches 325; Conservative 75; Mismatches 104; Indels 41; Gaps 8;
QY 2 MSRDTKTESQ-----SQSGTSSSSSSSAPQSYSSSS--SSGT 36
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
1 MSRESDEVAQSHGSSACSQPHGSVTQSGSSSSQSGISSSTSTMPNS-SQSSHPSSGT 59
QY 37 LSSLDTPVPQDLASI-----PEDPEIDEDIPOPWRLWALGKGLHNDCLHEEYVFGDK 91
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
60 LSSLETVSTQELYSIPEDQEPEDQEPETPAPARLWALQDGFANLSCVNDNVNWFGRDK 119
QY 92 KCDYTFDIPVLNQDRTYKTKSRHFRIFQELGHGHSRVANIEDLSNGTGFVNKEIIGKGR 151
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
120 SCEYCFDEPFLKRTGKRTYKSKGHFRIFREVPKNSYIAYIEDHSGNGTFVNTLGVGK 179
QY 152 TLPLTNNAEIALSLPTNKKVVFSDLVDDQTIYPKDFIDKYIMSRPIGSGACGEVKLAFQ 211
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
180 RPLNNSEIALSLSRNKVVFVFDLTVDQSVYKPEURDEYIMSKTIGSGACGEVKLAF 239
QY 212 KSVCKVAVKIISSKRKFMMNTSSNEHP-ISVDTEIEILKLDHPDIIKIENFFDSEDFY 270
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
240 RKTCKVAVKIISSKRKFPAIGSAREADPALNVETEIEILKLNHPCLIIKKNFFDAED-Y 298
QY 271 IVLEMEGGELDFRVVNSTRLEPIAKLYFYQMLLAQVYLHENGVIHRDLKPENVLSSST 330
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
299 IVLEMEGGELFDKVVGNKRLKEATCKLYFYQMLLAQVYLHENGIIHRDLKPENVLSSQ 358
QY 331 SEBCCIKITDQSGKILGETSLMRTLCTGTPPYLAPEVLNTAGTGYSSAVDCWSLGVTLF 390
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
359 EEDCLIKITDQSGKILGETSLMRTLCTGTPPYLAPEVLNVGTAGYGRVDCWSLGVTLF 418
QY 391 VCLCGYPPFSEQNSIPLKNQIAEGKYTYIAAAWRNVSEQAFDLVKLLVDPPEQLRTTK 450
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
419 ICLSGYPPFSEHRTQVSLKDQITSGKYNFIPEVWAEVSEKALDLVKLLVDPDKARFTTE 478
QY 451 QALEHFWLQDDSMKHTVERLMYGVDMHTMPP-----IKNIIRKRGHEWDQDASTSS----- 502
Db ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
479 EALRHPWLQDEDMKRFQDILLSENESTALPQVLAQFSTSRKRPRGEAGAEFTTKRPAV 538
QY 503 CSEIL 507
Db : : : : :
539 CAAVL 543
RESULT 8
US-10-820-583A-3
; Sequence 3, Application US/10820583A
; Publication No. US20040242461A1

```
; GENERAL INFORMATION:
; APPLICANT: Schneider, Michael
; TITLE OF INVENTION: Modulators of Telomere Stability
; FILE REFERENCE: HO-P02673US1
; CURRENT APPLICATION NUMBER: US/10/820,583A
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 60/461,095
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Human
US-10-820-583A-3

Query Match      55.3%; Score 1499; DB 16; Length 514;
Best Local Similarity 55.5%; Pred. No. 66-103;
Matches 302; Conservative 72; Mismatches 102; Indels 68; Gaps 8;

QY  2 MSRDYKTESQ-----QSGTSSSSSSSSAP-QSYSSSSSSGTL 37
Db  1 MSRESDEVAQSHGSSACSQPHGVTQSGSSSQSGISSSTSTWPNSSQSSSSGTL 60
QY  38 SSDLTVVQDLASI-----PEDPEIDEDIPQWGRMLWALGKGLFNLHDCLEHBYVFGROKK 92
Db  61 SSLETVSTQELYSIPEDQPEQPEPTPAWRLWALQDGFANLECVNDVNYFGRDKS 120
QY  93 CDYTEDIPVLOTDRYKTKYKSHFRIFQELGHGSRVANIEDLSNGTFFVKEIIGKRT 152
Db  121 CYCFDEPLLRKTRDYRTYKSHFRIFREVGPKNSYIAYIEDHSGNGTFFVNTLVGKGR 180
QY  153 LPLTNNAETALSLPTNKKVVFVSDLSVDDOTIYPKDFIDKYIMSRPTGSGACGEVKLAFQK 212
Db  181 RPLNNSEIALSLSRNKVVFVFDLTVDQDSVTPKALRDEYIMSKTLGSGACGEVKLAFER 240
QY  213 SVCKVAVKIIISKRKPKMNTSNEHP-ISVDTEIELKLDHPCIIKIENFDSDFYI 271
Db  241 KTKCKVAIKIISKRKFAIGSAREADPALNVETEIELKLDHPCIIKIKNFFDAED-YVI 299
QY  272 VLELMGGGLFDRVNSTELRPIAKLYEQMLLAVQYLHENGVIHRLDKPENVLSSSTS 331
Db  300 VLELMGGGLFDKVVGNKKEATCKLYFYQMLLAVQ-----336
QY  332 EECCIKITFGOSKILGETSLMRTLCGTPTYLAPVLANTAGTYSSAVDCMSLGVILFV 391
Db  337 -----ITDFGHSKILGETSLMRTLCGTPTYLAPVLVSVGTAGYNRAVDCMSLGVILFI 390
QY  392 CLCGYPPFSEQNSNIPKLNQIAEGKYTYIAAAWRNVSEQAFLVKNLLVVDPEQLRTTKQ 451
Db  391 CLSGYPPFSEHRTQVSLKDQITSGKYNFPEVMAEVSEKALDLVKKLLVVDPKARFTTEE 450
QY  452 ALEHHPLODSSMKHTVERLMYGVDDHTMPP-----IKNNIIRKRGHEWDQDASTSS-----C 503
Db  451 ALRHPWLODEMKRKFQDILLSEENESTALPQVLAQPSSTSRKRPREGEAETTKRPAYC 510
QY  504 SETL 507
Db  511 AAVL 514

RESULT 9
US-10-881-124A-9
; Sequence 9, Application US/10881124A
; Publication No. US20050112746A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysam, Stephen S.
; APPLICANT: Hendle, Jorg
; APPLICANT: Louis, Gordon V.
; TITLE OF INVENTION: Crystals and Structures of Protein Kinase CHK2
; FILE REFERENCE: 022132-001210US
; CURRENT APPLICATION NUMBER: US/10/881,124A
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/484,389
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/509,781
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted sequence of CHK2KD expressed protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: serine at position 1 is phosphorylated
```

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; CURRENT APPLICATION NUMBER: US/10/881,124A
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/484,389
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/509,781
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-881-124A-9

Query Match      40.4%; Score 1096.5; DB 17; Length 326;
Best Local Similarity 64.8%; Pred. No. 3e-73;
Matches 210; Conservative 43; Mismatches 66; Indels 5; Gaps 3;

QY  180 DOTYPKDFIDKYIMSRPTGSGACGEVKLAFQKSVCKVAVKIISKRKPKMNTSNEHP- 238
Db  3 DQSVYPKALRDEYIMSKTLGSGACGEVKLAFERKTKKVAIKIISKRKFAIGSAREADPA 62
QY  239 ISVDTEIELKLDHPCIIKIENFDSDFYIVLELMGGGLFDRVNSTELRPIAKL 298
Db  63 LNVETEIELKLDHPCIIKIKNFFDAED-YVIIVLELMGGGLFDKVVGNKKEATCKL 121
QY  299 YFYQMLLAVQYLHENGVIHRLDKPENVLSSTSSEBCCIKITDQSGKILGETSLMRTLCG 358
Db  122 YFYQMLLAVQYLHENGVIHRLDKPENVLSSQEECLKITDQFGHSKILGETSLMRLDLCG 181
QY  359 TPTYLAPVLANTAGTYSSAVDCMSLGVILFVCLCGYPPFSEQNSNIPKLNQIAEGKYT 418
Db  182 DPTYLAPVLVSVGTAGYNRAVDCMSLGVILFICLSGYPPFSEHRTQVSLKDQITSGKN 241
QY  419 YIAAAWRNVSEQAFLVKNLLVVDPEQLRTTKQALEHHPLODSSMKHTVERLMYGVDDHTM 478
Db  242 FIPEVMAEVSEKALDLVKKLLVVDPKARFTTEALRHPWLODEMKRKFQDILLSEENEST 301
QY  479 PPP---IKNNIIRKRGHEWDQDAS 499
Db  302 ALPQVLAQPSSTSRKRPREGEAEGA 325

RESULT 10
US-10-881-124A-8
; Sequence 8, Application US/10881124A
; Publication No. US20050112746A1
; GENERAL INFORMATION:
; APPLICANT: Structural Genomix, Inc.
; APPLICANT: Antonysam, Stephen S.
; APPLICANT: Hendle, Jorg
; APPLICANT: Louis, Gordon V.
; TITLE OF INVENTION: Crystals and Structures of Protein Kinase CHK2
; FILE REFERENCE: 022132-001210US
; CURRENT APPLICATION NUMBER: US/10/881,124A
; CURRENT FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/484,389
; PRIOR FILING DATE: 2003-07-01
; PRIOR APPLICATION NUMBER: US 60/509,781
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Predicted sequence of CHK2KD expressed protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: serine at position 1 is phosphorylated
```


QY 380 VDCWSGLVILFVCLGYPPESEONSIPLKNOIAEGKTYTIAAARNVSEQAFDLVKNLL 439
 Db 402 VDLWSAGVILVCLGYPPESDGPGPSLKEQLQAKYAFISPYWDKIDDSVLHLISNLL 461
 QY 440 VVDPEQLTTKQALEHPWLQD-----DSMKHTVERLMYGVDMHTMP 479
 Db 462 VLNPDERYNIDEALNHPWFNDIQQSSVSLELQRLQI-TDNKIP 504

RESULT 13

US-09-733-388-4
 ; Sequence 4, Application US/09733388
 ; Publication No. US2003006495A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Greg
 ; APPLICANT: Scoville, John
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Abuin, Alejandro
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and
 ; FILE REFERENCE: Lex-0103-USA
 ; CURRENT APPLICATION NUMBER: US/09/733,388
 ; CURRENT FILING DATE: 2000-12-07
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-733-388-4

Query Match 22.2%; Score 603; DB 10; Length 356;
 Best Local Similarity 38.1%; Pred. No. 1.7e-36;
 Matches 128; Conservative 62; Mismatches 106; Indels 40; Gaps 6;

QY 198 IGSAGCEVVKLAFQKSVCKKAVAKIISKRFKMTSSNEHPISVDTEIELKKLDHPCII 257
 Db 29 LGTGAFSEVVLAEKATGKLFVAKCTPKALKGKES-----SIENEIAVLRIKHENIV 82
 QY 258 KIENFFDSEDFYIVLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQVYLHENGVIH 317
 Db 83 ALEDIVESPNHLYVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDVAVYLLHRMGIVH 142
 QY 318 RDLKPNVLLSSTSECCIKITDFGQSKILGTSMLRTLCGTPTYLAPEVLNLTAGTTGYS 377
 Db 143 RDLKPNLLYYSODEESKIMISDFGLSKMEGKGDVMTAGTGPYVAPEVL---AQKPY 199
 QY 378 SAVDCWSGLVILFVCLGYPPESEONSIPLKNOIAEGKTYTIAAARNVSEQAFDLVKN 437
 Db 200 KAVDCWSIGVIAVILCGYPPEFYDENDS-KLFEQILKAIEYFDPYWDIDISAKDFIRN 258
 QY 438 LLVVDPEQLTTKQALEHPWLQDSSMKHTVERLMYGVDMHTMPPIKNIIRKRGHEWDO- 496
 Db 259 LMEKDPNKRYTCQAAHPHPIADTALNKNIH-----ESVSAQIRKNFAKSK---WROA 308
 QY 497 -----DASTSSCSEILPTSAEK 513
 Db 309 FNATAVVRHMRKHLGSSLDSSNASVSSSLASQK 344

RESULT 14

US-10-446-175-4
 ; Sequence 4, Application US/10446175
 ; Publication No. US2004001412A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Greg
 ; APPLICANT: Scoville, John
 ; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Abuin, Alejandro
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: No. US2004001412A1el Human Kinase Proteins and
 ; FILE REFERENCE: Lex-0103-USA
 ; CURRENT APPLICATION NUMBER: US/10/446,175
 ; CURRENT FILING DATE: 2003-05-27
 ; PRIOR FILING DATE: US/09/733,388
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 356
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-446-175-4

Query Match 22.2%; Score 603; DB 15; Length 356;
 Best Local Similarity 38.1%; Pred. No. 1.7e-36;
 Matches 128; Conservative 62; Mismatches 106; Indels 40; Gaps 6;
 QY 198 IGSAGCEVVKLAFQKSVCKKAVAKIISKRFKMTSSNEHPISVDTEIELKKLDHPCII 257
 Db 29 LGTGAFSEVVLAEKATGKLFVAKCTPKALKGKES-----SIENEIAVLRIKHENIV 82
 QY 258 KIENFFDSEDFYIVLELMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQVYLHENGVIH 317
 Db 83 ALEDIVESPNHLYVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDVAVYLLHRMGIVH 142
 QY 318 RDLKPNVLLSSTSECCIKITDFGQSKILGTSMLRTLCGTPTYLAPEVLNLTAGTTGYS 377
 Db 143 RDLKPNLLYYSODEESKIMISDFGLSKMEGKGDVMTAGTGPYVAPEVL---AQKPY 199
 QY 378 SAVDCWSGLVILFVCLGYPPESEONSIPLKNOIAEGKTYTIAAARNVSEQAFDLVKN 437
 Db 200 KAVDCWSIGVIAVILCGYPPEFYDENDS-KLFEQILKAIEYFDPYWDIDISAKDFIRN 258
 QY 438 LLVVDPEQLTTKQALEHPWLQDSSMKHTVERLMYGVDMHTMPPIKNIIRKRGHEWDO- 496
 Db 259 LMEKDPNKRYTCQAAHPHPIADTALNKNIH-----ESVSAQIRKNFAKSK---WROA 308
 QY 497 -----DASTSSCSEILPTSAEK 513
 Db 309 FNATAVVRHMRKHLGSSLDSSNASVSSSLASQK 344

RESULT 15

US-10-936-445-4
 ; Sequence 4, Application US/10936445
 ; Publication No. US20050079530A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Donoho, Greg
 ; APPLICANT: Scoville, John
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Friedrich, Glenn
 ; APPLICANT: Zambrowicz, Brian
 ; APPLICANT: Abuin, Alejandro
 ; APPLICANT: Sands, Arthur T.
 ; TITLE OF INVENTION: Novel Human Kinase Proteins and
 ; FILE REFERENCE: Lex-0103-USA
 ; CURRENT APPLICATION NUMBER: US/10/936,445
 ; CURRENT FILING DATE: 2004-09-08
 ; PRIOR FILING DATE: US/10/446,175
 ; PRIOR FILING DATE: 2003-05-27
 ; PRIOR FILING DATE: 1999-12-07
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 356
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-936-445-4

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; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-936-445-4

Query Match      22.2%; Score 603; DB 17; Length 356;
Best Local Similarity 38.1%; Pred. No. 1.7e-36;
Matches 128; Conservative 62; Mismatches 106; Indels 40; Gaps 6;

Qy      198 IGSGACGEVKLAFQSKVCKVAVKIIISKRRFPKMTSSNEHPISVDTEIILKLDHPCHII 257
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      29 LGTGAFSEVLLAEKATGKLFVAKCI PKKALKGKES-----STENIAVLARKIKHENIV 82

Qy      258 KIENFFDSEDFYIYLVLEMGEGELFDRVNSTRLREPIAKLYFTQMLLAVOYLHENGVIH 317
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      83 ALEDIYESPNHLYLVMLQVSGGELFDRIVEKGFYTERKDASTLIIRQVLDAVYILHRMGIVH 142

Qy      318 RDLKPENVLVLSSTSEECIKITDFGQSKILGETSLMRTCLGCTPYLAPELVNTAGTTGYS 377
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      143 RDLKPENLVYSQDEESKIMISDFGLSKMEGKGVNSTACGTPGYVAPEVL---AQRPYS 199

Qy      378 SAVDCWSGLVILFVCLGCGYPPFSQNSNIPUKNOIAEGKYTYIAAAWRNVSEQAFLDVKN 437
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      200 KAVDCWSIGVIATYLLCGYPPFYDENDS-KLFEQILKAEEYFDSFYDDIDSASAKDFIRN 258

Qy      438 LLVVDPEQRLLTKQALEHPMLQDDSMKHTVERLMYGVDHTMPPPIKKNILIRKRGHEWDO- 496
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      259 LMEKDPNKRITYCEQAARHPVIADTALNKNTH-----ESVSAQIRKNFAKSK---WRQA 308

Qy      497 -----DASTSSCEILPTSAEK 513
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      309 FNATAVVHRMRKHLGSLDSSNNAVSSSLSLQSK 344

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Search completed: July 7, 2005, 13:06:39
Job time : 165 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2712	100.0	517	4	US-09-849-617-2	Sequence 2, Appli
2	1855.5	61.0	543	4	US-09-529-093A-2	Sequence 2, Appli
3	1855.5	61.0	543	4	US-09-529-154-2	Sequence 2, Appli
4	1589.5	58.6	490	4	US-09-949-016-10788	Sequence 10788, A
5	603	22.2	356	4	US-09-733-388-4	Sequence 4, Appli
6	603	22.2	356	4	US-10-446-175-4	Sequence 4, Appli
7	600.5	22.1	355	4	US-09-579-664B-10	Sequence 10, Appl
8	600.5	22.1	355	4	US-10-355-975A-10	Sequence 10, Appl
9	600.5	22.1	385	4	US-09-733-388-2	Sequence 2, Appli
10	600.5	22.1	385	4	US-10-446-175-2	Sequence 2, Appli
11	591.5	21.8	370	2	US-08-678-989-19	Sequence 19, Appl
12	591.5	21.8	370	3	US-09-272-796-19	Sequence 19, Appl
13	591.5	21.8	370	3	US-09-457-040B-31	Sequence 31, Appl
14	591.5	21.8	370	4	US-09-538-092-1314	Sequence 1314, Ap
15	591.5	21.8	415	4	US-09-949-016-7461	Sequence 7461, Ap
16	591.5	21.8	415	4	US-09-949-016-7462	Sequence 7462, Ap
17	580.5	21.4	476	4	US-09-960-643-2	Sequence 2, Appli
18	575.5	21.2	776	1	US-08-198-446B-17	Sequence 17, Appl
19	575.5	21.2	776	2	US-08-870-693-17	Sequence 17, Appl
20	575.5	21.2	821	1	US-08-198-446B-6	Sequence 6, Appli
21	575.5	21.2	821	2	US-08-870-693-6	Sequence 6, Appli
22	559	20.6	513	4	US-09-248-796A-18515	Sequence 18515, A
23	531	19.6	473	4	US-09-538-092-1353	Sequence 1353, Ap
24	527	19.4	384	4	US-09-230-896C-29	Sequence 29, Appl
25	525.5	19.4	456	1	US-08-464-164-2	Sequence 2, Appli
26	525.5	19.4	456	1	US-08-338-057-2	Sequence 2, Appli
27	525.5	19.4	456	2	US-08-668-416-2	Sequence 2, Appli

QY 361 TYLAPEVLNLTAGTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLNQIAEGKYIYI 420
DB 361 TYLAPEVLNLTAGTGYSSAVDCWSLGVILFVCLCGYPPFSEQNSNIPLNQIAEGKYIYI 420
QY 421 AAARNVSEQAQDLVKNLLVDPDEQLTTKQALEHPWLQDDSMKHTVERLMTGVDPHTMPP 480
DB 421 AAARNVSEQAQDLVKNLLVDPDEQLTTKQALEHPWLQDDSMKHTVERLMTGVDPHTMPP 480
QY 481 PIKKNIIIRKRGHEWDQDASTSSCSEILPTSAEKRAK 517
DB 481 PIKKNIIIRKRGHEWDQDASTSSCSEILPTSAEKRAK 517

RESULT 2
US-09-529-093A-2
; Sequence 2, Application US/09529093A
; Patent No. 6413755
; GENERAL INFORMATION:
; APPLICANT: LUYTEN, Walter H.M.L.
; APPLICANT: PARKER, Andrew E.
; APPLICANT: MCGOWAN, Clare H.
; APPLICANT: BLASINA, Alessandra
; TITLE OF INVENTION: Human Checkpoint Kinase, hCDS1, Compositions and Methods
; FILE REFERENCE: TSRI 649.0
; CURRENT APPLICATION NUMBER: US/09/529,093A
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/EP98/06981
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: GB 9722320.0
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-093A-2

Query Match 61.0%; Score 1655.5; DB 4; Length 543;
Best Local Similarity 59.9%; Pred. No. 9e-152;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTESQ-----QSOGTSSSSSSSAP-QSYSSSSSSGTL 37
DB 1 MSRESDEVAQSHGSSACSQPHGVSQTQSGSSSQSGISSSTSTMPNSSQSSSSGTL 60
QY 38 SSDLTVVPQDLASI-----PEDPEIDEDIPQWGRWLWALGKFLNHDCLHBEYVFGDKK 92
DB 61 SSLETVSTQELYSIPEDQEPEDQEPPEPTAPWRLWALQDGFANLECVDNDYWFGRDKS 120
QY 93 CDYTFDIPVLNQTDRYKTSKHFRIFOELGHGHSRVANIEDLSGNGTFFVKEIIGKRT 152
DB 121 CEYCFDEPLLRKTRDKYRTYSKKHFRIFREVGPKNSYIAYIEDHSGNGTFFVNTLVGKGR 180
QY 153 LPLTNNAEIALSLPTNKVVFSDLSVDDOTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
DB 181 RPLNNNSIALSLRNKRVFFDLTVDDQSVYPKALRDEYIMSKTLGSGACGEVKLAFER 240
QY 213 SVCKKVAVKIISKRFKMTSSNEHP-ISVDTEIELKLDHPICIIKIENFFDSDFYI 271
DB 241 KTCCKVAIKIISKRFKAIGSAREADPALNVETEIELKLNHPICIIKKNFFDAED-YI 299
QY 272 VLEMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRLDKPENVLSSSTS 331
DB 300 VLEMEGGELFDKVGNGKRLKEATCKLYFYQMLLAVQYLHENGIIHRLDKPENVLSSSQE 359
QY 332 BECCIKITDFGSKILGETSLMRTLCTGPTTYLAPEVLNLTAGTGYSSAVDCWSLGVILFV 391
DB 360 EDCLIKITDFGSKILGETSLMRTLCTGPTTYLAPEVLNLTAGTGYSSAVDCWSLGVILFI 419
QY 392 CLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAQDLVKNLLVDPDEQLTTKQ 451
DB 420 CLSGYPPFSEHRTQVSLKDQITSGKYNFIPVMAEVSEKALDVKLLVDPKARFTTEE 479
QY 452 ALEHPWLQDDSMKHTVERLMTGVDPHTMPP-----TKNNIIIRKRGHEWDQDASTSS-----C 503
DB 480 ALRHPWLQDEDMKRFQDLLSEENESTALPQVLAQPSRKRPRGEAEGAEATTTKRPAVC 539

QY 452 ALEHPWLQDDSMKHTVERLMTGVDPHTMPP-----TKNNIIIRKRGHEWDQDASTSS-----C 503
DB 480 ALRHPWLQDEDMKRFQDLLSEENESTALPQVLAQPSRKRPRGEAEGAEATTTKRPAVC 539
QY 504 SEIL 507
DB 540 AAVL 543
RESULT 3
US-09-529-154-2
; Sequence 2, Application US/09529154
; Patent No. 6531312
; GENERAL INFORMATION:
; APPLICANT: LUYTEN, Walter H.M.L.
; APPLICANT: PARKER, Andrew E.
; TITLE OF INVENTION: A NOVEL HUMAN CHECKPOINT KINASE, hCDS1, COMPOSITIONS
; FILE REFERENCE: JAB 1333 (US)
; CURRENT APPLICATION NUMBER: US/09/529,154
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: PCT/EP98/06982
; PRIOR FILING DATE: 1998-10-21
; PRIOR APPLICATION NUMBER: GB 9722320.0
; PRIOR FILING DATE: 1997-10-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-529-154-2

Query Match 61.0%; Score 1655.5; DB 4; Length 543;
Best Local Similarity 59.9%; Pred. No. 9e-152;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;
QY 2 MSRDTKTESQ-----QSOGTSSSSSSSAP-QSYSSSSSSGTL 37
DB 1 MSRESDEVAQSHGSSACSQPHGVSQTQSGSSSQSGISSSTSTMPNSSQSSSSGTL 60
QY 38 SSDLTVVPQDLASI-----PEDPEIDEDIPQWGRWLWALGKFLNHDCLHBEYVFGDKK 92
DB 61 SSLETVSTQELYSIPEDQEPEDQEPPEPTAPWRLWALQDGFANLECVDNDYWFGRDKS 120
QY 93 CDYTFDIPVLNQTDRYKTSKHFRIFOELGHGHSRVANIEDLSGNGTFFVKEIIGKRT 152
DB 121 CEYCFDEPLLRKTRDKYRTYSKKHFRIFREVGPKNSYIAYIEDHSGNGTFFVNTLVGKGR 180
QY 153 LPLTNNAEIALSLPTNKVVFSDLSVDDOTIYPKDFIDKYIMSRPIGSGACGEVKLAFQK 212
DB 181 RPLNNNSIALSLRNKRVFFDLTVDDQSVYPKALRDEYIMSKTLGSGACGEVKLAFER 240
QY 213 SVCKKVAVKIISKRFKMTSSNEHP-ISVDTEIELKLDHPICIIKIENFFDSDFYI 271
DB 241 KTCCKVAIKIISKRFKAIGSAREADPALNVETEIELKLNHPICIIKKNFFDAED-YI 299
QY 272 VLEMEGGELFDRVNVNSTRLEPIAKLYFYQMLLAVQYLHENGVIHRLDKPENVLSSSTS 331
DB 300 VLEMEGGELFDKVGNGKRLKEATCKLYFYQMLLAVQYLHENGIIHRLDKPENVLSSSQE 359
QY 332 BECCIKITDFGSKILGETSLMRTLCTGPTTYLAPEVLNLTAGTGYSSAVDCWSLGVILFV 391
DB 360 EDCLIKITDFGSKILGETSLMRTLCTGPTTYLAPEVLNLTAGTGYSSAVDCWSLGVILFI 419
QY 392 CLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAQDLVKNLLVDPDEQLTTKQ 451
DB 420 CLSGYPPFSEHRTQVSLKDQITSGKYNFIPVMAEVSEKALDVKLLVDPKARFTTEE 479
QY 452 ALEHPWLQDDSMKHTVERLMTGVDPHTMPP-----TKNNIIIRKRGHEWDQDASTSS-----C 503
DB 480 ALRHPWLQDEDMKRFQDLLSEENESTALPQVLAQPSRKRPRGEAEGAEATTTKRPAVC 539


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; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-175-4

Query Match      22.1%; Score 603; DB 4; Length 356;
Best Local Similarity 38.1%; Pred. No. 7.7e-50;
Matches 128; Conservative 62; Mismatches 106; Indels 40; Gaps 6;

QY 198 IGSAGCEVKLAFQKSVCKKVAVKIISKRFKMTSSNEHPISVDTEIILKLDHPICII 257
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
29 LGTGAFSEVVLAEKATGKLFVAKCIPKALKGKES-----SIENEIAVLKIKHENIV 82
QY 258 KIENPFDSDFYIIVLELMGEGELFDRVNVNSTRLEPIAKLYFYQMLLAVQVYLHENGVIH 317
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
83 ALEDIYESPNHLYLVMLVQVSGGELFDRIVEKGFYTEKDASTLIQVLDVAVYLRHMGIVH 142
QY 318 RDLKPNVLLSTSECCIKITDFQSKILGETSLMRTLCTGPTTYLAPEVLNAGTGTGYS 377
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
143 RDLKPNVLLSYSDSESKIMISDFGLSKMEGKGDVMTACGTPGYVAPEVL---AQKPY 199
QY 378 SAVDCWSLGVILFVCLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAFLVKN 437
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
200 KAVDCWSIGVIAYILLCGYPFFYDENDS-KLFEQILKAEYEFDSYPWDDISDAKDFIRN 258
QY 438 LLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDDHTMPPPIKNIIRKRGHEWDO- 496
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
259 LMEKDPNKRYTCEQAARHPWTAGDT-----ALSKNIHESVSAQIRKNFAKSK---WRQA 308
QY 497 -----DASTSCSEILPTSAAK 513
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
309 FNATAVVRHMRRLQLGSSLDSSNASVSSLSASOK 344

RESULT 7
US-09-579-664B-10
; Sequence 10, Application US/09579664B
; Patent No. 6514719
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES
; FILE REFERENCE: 2923-A
; CURRENT APPLICATION NUMBER: US/09/579,664B
; CURRENT FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-579-664B-10

Query Match      22.1%; Score 600.5; DB 4; Length 355;
Best Local Similarity 38.4%; Pred. No. 1.3e-49;
Matches 129; Conservative 61; Mismatches 107; Indels 39; Gaps 6;

QY 198 IGSAGCEVKLAFQKSVCKKVAVKIISKRFKMTSSNEHPISVDTEIILKLDHPICII 257
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
29 LGTGAFSEVVLAEKATGKLFVAKCIPKALKGKES-----SIENEIAVLKIKHENIV 82
QY 258 KIENPFDSDFYIIVLELMGEGELFDRVNVNSTRLEPIAKLYFYQMLLAVQVYLHENGVIH 317
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
83 ALEDIYESPNHLYLVMLVQVSGGELFDRIVEKGFYTEKDASTLIQVLDVAVYLRHMGIVH 142
QY 318 RDLKPNVLLSTSECCIKITDFQSKILGETSLMRTLCTGPTTYLAPEVLNAGTGTGYS 377
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
143 RDLKPNVLLSYSDSESKIMISDFGLSKMEGKGDVMTACGTPGYVAPEVL---AQKPY 199
QY 378 SAVDCWSLGVILFVCLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAFLVKN 437
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
200 KAVDCWSIGVIAYILLCGYPFFYDENDS-KLFEQILKAEYEFDSYPWDDISDAKDFIRN 258
QY 438 LLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDDHTMPPPIKNIIRKRGHEWDO- 496
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
259 LMEKDPNKRYTCEQAARHPWTAGDT-----ALSKNIHESVSAQIRKNFAKSK---WRQA 308
QY 497 -----DASTSCSEILPTSAAK 513
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
309 FNATAVVRHMRRLQLGSSLDSSNASVSSLSASOK 344

RESULT 9
US-09-733-388-2
; Sequence 2, Application US/09733388
; Patent No. 6602698
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QY 318 RDLKPNVLLSTSECCIKITDFQSKILGETSLMRTLCTGPTTYLAPEVLNAGTGTGYS 377
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143 RDLKPNVLLSYSDSESKIMISDFGLSKMEGKGDVMTACGTPGYVAPEVL---AQKPY 199
QY 378 SAVDCWSLGVILFVCLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAFLVKN 437
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
200 KAVDCWSIGVIAYILLCGYPFFYDENDS-KLFEQILKAEYEFDSYPWDDISDAKDFIRN 258
QY 438 LLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDDHTMPPPIKNIIRKRGHEWDO- 496
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
259 LMEKDPNKRYTCEQAARHPWTAGDT-----ALSKNIHESVSAQIRKNFAKSK---WRQA 309
QY 497 -----DASTSCSEILPTSAAK 513
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
310 FNATAVVRHMRRLQLGSSLDSSNASVSSNLASOK 345

RESULT 8
US-10-355-975A-10
; Sequence 10, Application US/10355975A
; Patent No. 6759223
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
; FILE REFERENCE: 2923-B
; CURRENT APPLICATION NUMBER: US/10/355,975A
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-355-975A-10

Query Match      22.1%; Score 600.5; DB 4; Length 355;
Best Local Similarity 38.4%; Pred. No. 1.3e-49;
Matches 129; Conservative 61; Mismatches 107; Indels 39; Gaps 6;

QY 198 IGSAGCEVKLAFQKSVCKKVAVKIISKRFKMTSSNEHPISVDTEIILKLDHPICII 257
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
29 LGTGAFSEVVLAEKATGKLFVAKCIPKALKGKES-----SIENEIAVLKIKHENIV 82
QY 258 KIENPFDSDFYIIVLELMGEGELFDRVNVNSTRLEPIAKLYFYQMLLAVQVYLHENGVIH 317
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
83 ALEDIYESPNHLYLVMLVQVSGGELFDRIVEKGFYTEKDASTLIQVLDVAVYLRHMGIVH 142
QY 318 RDLKPNVLLSTSECCIKITDFQSKILGETSLMRTLCTGPTTYLAPEVLNAGTGTGYS 377
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
143 RDLKPNVLLSYSDSESKIMISDFGLSKMEGKGDVMTACGTPGYVAPEVL---AQKPY 199
QY 378 SAVDCWSLGVILFVCLCGYPPFSEQNSNIPLNQIAEGKYTYIAAARNVSEQAFLVKN 437
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200 KAVDCWSIGVIAYILLCGYPFFYDENDS-KLFEQILKAEYEFDSYPWDDISDAKDFIRN 258
QY 438 LLVVDPEQRLTTKQALEHPWLQDDSMKHTVERLMYGVDDHTMPPPIKNIIRKRGHEWDO- 496
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
259 LMEKDPNKRYTCEQAARHPWTAGDT-----ALSKNIHESVSAQIRKNFAKSK---WRQA 309
QY 497 -----DASTSCSEILPTSAAK 513
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
310 FNATAVVRHMRRLQLGSSLDSSNASVSSNLASOK 345

RESULT 9
US-09-733-388-2
; Sequence 2, Application US/09733388
; Patent No. 6602698
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Query Match 21.8%; Score 591.5; DB 3; Length 370;
Best Local Similarity 39.9%; Pred. No. 1.1e-48;
Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;

QY 186 KPFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRFKMTSSNEHPISVDTEI 245
DB 14 EDIRDIYDFRDVLGTGAFSEVILAEKRTQKLVAKIAKEALEGEGSMEN-----EI 67

QY 246 EILKLDHPCIIKIENFFDSEDFYIVLELMEGGEFDRVNVNSTRLEPIAKLYFYQMLL 305
DB 68 AVLHKIKHPNIVALDDIYESGGHLYIMQLVSGGEFDRIVEKGFYTERDASRLIFQVLD 127

QY 306 AVOYLHENGVIHRDLKPNVLLSSTSECCIKITDFGQSKILGETSLMRTLCTPTYLAP 365
DB 128 AVKYLHDLGIVHRDLKPNLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTGYPVAP 187

QY 366 EVLNTAGTGYSSAVDCWSLGVTLFVCLCGYPPFSEQNSNIPKNOIAEGKTYTAAAWR 425
DB 188 EYL---AQPKYSKAVDCWSIGVAYILLCGYPPFYDEN-DAKLFEQILKAEYEFDSPYWD 243

QY 426 NVSEQAFDLVKNLLVVDPEORLTQKALEHPWLQDDSMKHTVERLMYGVDMTPPPIKKN 485
DB 244 DISDSAKDFIRHLMKEDPEKRTCEQALQHPWIAGDT-----ALDKNIHQSVSEQIKKN 297

QY 486 IIRKRGHEWDQ 496
DB 298 FAKSK---WKQ 305

RESULT 14
US-09-538-092-1314
; Sequence 1314, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1314
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)_(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14012

Query Match 21.8%; Score 591.5; DB 4; Length 370;
Best Local Similarity 39.9%; Pred. No. 1.1e-48;
Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;

QY 186 KPFIDKYIMSRPIGSGACGEVKLAFQKSVCKKVAVKIISKRFKMTSSNEHPISVDTEI 245
DB 14 EDIRDIYDFRDVLGTGAFSEVILAEKRTQKLVAKIAKEALEGEGSMEN-----EI 67

QY 246 EILKLDHPCIIKIENFFDSEDFYIVLELMEGGEFDRVNVNSTRLEPIAKLYFYQMLL 305
DB 68 AVLHKIKHPNIVALDDIYESGGHLYIMQLVSGGEFDRIVEKGFYTERDASRLIFQVLD 127

QY 306 AVOYLHENGVIHRDLKPNVLLSSTSECCIKITDFGQSKILGETSLMRTLCTPTYLAP 365
DB 128 AVKYLHDLGIVHRDLKPNLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTGYPVAP 187

QY 366 EVLNTAGTGYSSAVDCWSLGVTLFVCLCGYPPFSEQNSNIPKNOIAEGKTYTAAAWR 425
DB 188 EYL---AQPKYSKAVDCWSIGVAYILLCGYPPFYDEN-DAKLFEQILKAEYEFDSPYWD 243

QY 426 NVSEQAFDLVKNLLVVDPEORLTQKALEHPWLQDDSMKHTVERLMYGVDMTPPPIKKN 485
DB 244 DISDSAKDFIRHLMKEDPEKRTCEQALQHPWIAGDT-----ALDKNIHQSVSEQIKKN 297

QY 486 IIRKRGHEWDQ 496
DB 298 FAKSK---WKQ 305

RESULT 15
US-09-949-016-7461
; Sequence 7461, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7461
; LENGTH: 415
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7461

Query Match 21.8%; Score 591.5; DB 4; Length 415;
Best Local Similarity 39.9%; Pred. No. 1.3e-48;
Matches 124; Conservative 61; Mismatches 107; Indels 19; Gaps 5;

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DB 59 EDIRDIYDFRDVLGTGAFSEVILAEKRTQKLVAKIAKEALEGEGSMEN-----EI 112

QY 246 EILKLDHPCIIKIENFFDSEDFYIVLELMEGGEFDRVNVNSTRLEPIAKLYFYQMLL 305
DB 113 AVLHKIKHPNIVALDDIYESGGHLYIMQLVSGGEFDRIVEKGFYTERDASRLIFQVLD 172

QY 306 AVOYLHENGVIHRDLKPNVLLSSTSECCIKITDFGQSKILGETSLMRTLCTPTYLAP 365
DB 173 AVKYLHDLGIVHRDLKPNLLYYSLDEDSKIMISDFGLSKMEDPGSVLSTACGTGYPVAP 232

QY 366 EVLNTAGTGYSSAVDCWSLGVTLFVCLCGYPPFSEQNSNIPKNOIAEGKTYTAAAWR 425
DB 233 EYL---AQPKYSKAVDCWSIGVAYILLCGYPPFYDEN-DAKLFEQILKAEYEFDSPYWD 288

QY 426 NVSEQAFDLVKNLLVVDPEORLTQKALEHPWLQDDSMKHTVERLMYGVDMTPPPIKKN 485
DB 289 DISDSAKDFIRHLMKEDPEKRTCEQALQHPWIAGDT-----ALDKNIHQSVSEQIKKN 342

QY 486 IIRKRGHEWDQ 496
DB 343 FAKSK---WKQ 350

Search completed: July 7, 2005, 13:03:49
Job time : 44 secs

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